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                                                                              DNA encoding novel human diagnostic protein #10627
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC considering expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations consisting for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC The polypeptide and polynucleotide sequences have applications in CC amino acid sequences. AAS64197-AAS94564 represent novel human CC amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC and to produce data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wince in the printed of the printed of the printed specification.
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Sequence
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                                                                                                                                                                                        P-PSDB;
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RESULT 4
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ID AAS26286 standard; cDNA; 983 BP.
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gtgctttagcctgaagtcaaaccttaaccaaacacca

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11-SEP-2000
01-SEP-2000
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2000US-0184664.
2000US-0184664.
2000US-0184664.
2000US-0184674.
2000US-019874.
2000US-0198123.
2000US-0299467.
2000US-0215135.
2000US-0215486.
2000US-0217486.
2000US-0217486.
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2000US-0217487.
2000US-02271487.
2000US-02271487.
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2000US-0227518.
2000US-0225267.
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2000US-0225688.
2000US-0225688.
2000US-0229343
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2000US-0229513
2000US-0230437
2000US-0231242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein,
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    08-SEP-2000
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2000US -0234274
2000US -0234997
2000US -0234988
2000US -0235834
2000US -0235836
2000US -0235369
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2000US-0232398.

2000US-02323400.

2000US-0232401.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC are also used in diagnosing a pathological condition or susceptibility Ct to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, CC cardiovascular disorders e.g. neoplasms of the breast or liver, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders (C. e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. CC alzheimer's disease, infections caused by bacteria, viruses and fungi CC and ocular disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC prevent skin aging due to sunburn, to maintain organs before CC transplantation, for supporting cell culture of primary tissues, to crederate tissues and in chemotaxis. The polypeptides can also be used CC as a food additive or preservative to increase or decrease storage can also the content of the polypeptides can also be used CC as a food additive or preservative to increase or decrease storage can be content to the content of the polypeptides can also be used CC as a food additive or preservative to increase or decrease storage can be content to the content of the content 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice rabbits, goats, horses, cats, dogs, chickens or sheep. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted diagnosing, preventing, treating or ameliorating medica used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capabilities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated nucleic acid molecules and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                         467
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750
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                   atgtccactggacctctgtccagaatcgaagccagaaattcaacttagtccctcctgccc
                                                                                                                                                                                         gcacagggaggtgatgctggagacttataaccatctggtctcactggaaattccatcttc
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atgtccactggacctctgtccanaatcgaagccagaaattcaacttagtccctcctgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                       encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                   ies, fat content, lipid, protein, carbohydrate, vitamins, cofactors and other nutritional components. The present encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
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2000US-0251988.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0254097.
2001US-0259678.
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2000US-0250160
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                                                                                                                                                                                                                                                                                                                                                        Score 231; DB 22; Pred. No. 2.4e-103;
                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT
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XX Huma
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                                                                                                                                                                                                             Query Match
Best Local Similarity 99.3
Matches 149; Conservative
                                                      2679
                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine, cell
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia, nervous
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ctgctgtgggggttggggaccactccctgcatcccctctccactgagagctgttcttttg
                                                                                                     ttcccctattctgagcccataaaagacccagactcagctgcagtgaggagagaaatcacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to human polynucleotides (AAI79941-AAI93841) and roteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation or cell differentiation or which may induce
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99.38;
                                                                                                                                                                                                                                                                                                                                              75 C; 93 G;
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                                                                                                                                                                                                                                         Score 99;
Pred. No.
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                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                           2.6e-38;
                                                                                                                                                                                                                                                                                                                                              Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system disorders,
                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                              Length 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                        part of the printed directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis and
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                                                                      Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                         site of a promoter, and not only the recruitment site of the promoter.

The method is used to: (a) identify a zinc finger domain that recognises a target site on a DNA; (b) determine whether a test zinc finger domain recognises a target site on a promoter; (c) generate a nucleic acid that encodes a chimeric zinc finger protein; and (d) identify DNA sequences recognised by zinc finger domains. The method can be used to design novel polypeptides that bind to a specific site on a DNA. The method can regulate the customised generation of new polypeptides that can regulate the customised generation of new polypeptides that can pathogen can be repressed, a gene required for cancerous growth can be repressed, a gene required for cancerous growth can be repressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-557644/62.
P-PSDB; AAU08514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a zinc finger domain for e.g. designing new polypeptides that bind to a specific site on a DNA, comprises expressing hybrid nucleic acids with a test zinc finger domain in cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of identifying a zinc finger domain that recognises a target site on a DNA. The medic comprises expressing hybrid nucleic acids with a test zinc finger domain in cells containing reporter construct, where the reporter gene is expressed above a given level when a transcription factor recognises a recruitment and a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2000; 2000KR-0007730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2001; 2001WO-KR00244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding zinc finger domain TG-ZFD-012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS13031 standard;
                                     1269
                                                                                                                                                           Sequence 69
                                                                                                                                                                                         coding sequence of TG-ZFD-012 zinc the method of the invention.
                                                                                                                                                                                                                           repressed, or a gene poorly expressed or encoding a mutated protein can be activated and overexpressed. The method can be used in vivo which enables identification of polypeptides that bind to a specific site on a bown in the intracellular milieu. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 22; Page 55; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOOL-) TOOLGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-DEC-2001
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                tatgtttgcagggaatgtgggcgtggctttcgccagcattcacaccctggtcagacacaag 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            finger domain; cancer; human; ds; TG-ZFD-012.
 tatgtttgcagggaatgtgggcgtggctttcgccagcattcacacctggtcagacacaag
                                                                         69;
                                                                                      Similarity
                                                                                                                                                           BP;
                                                                        Conservative
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                                                                                                                                                           17 A; 16 C;
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100.0%; Pr
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                                                                      Score 69; DB Pred. No. 1.6
                                                                                                                                                           20 G;
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                                                                                                                                                                                                           finger protein which was used in
                                                                                                                                                           Τ;
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                                                                                        1.6e-23;
                                                                                                        DB 22;
                                                                                                                                                           other;
                                                                                                    Length 69
                                                                        Indels
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Query Match Best Local Matches

. Similarity 100 69; Conservative

2.5%;

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Score 69; DB Pred. No. 1.6 0; Mismatches

1.6e-23; hes 0; DB 22;

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Gaps

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Length 69 Indels

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RESULT
AAS13088
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                                                                                                                                         site of a promoter, and not only the recruitment site of the promoter. The method is used to: (a) identify a zinc finger domain that recognise a target site on a DNA; (b) determine whether a test zinc finger domain recognises a target site on a promoter; (c) generate a nucleic acid that encodes a chimeric zinc finger protein; and (d) identify DNA sequences recognised by zinc finger domains. The method can be used to design now polypeptides that bind to a specific site on a DNA. The method can polypeptides that bind to a specific site on a DNA. The method can regulate the customised generation of new polypeptides that can regulate the customised generation of new polypeptides that can pathogen can be repressed, a gene required for cancerous growth can be pathogen can be repressed, a gene required for cancerous growth can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1329 aggacacat
                                  repressed, or a gene poorly expressed or encoding a mutated protein car be activated and overexpressed. The method can be used in vivo which enables identification of polypeptides that bind to a specific site on DNA in the intracellular milieu. The present sequence represents the coding sequence of TG-ZFD-046 zinc finger protein which was used in the method of the invention.
                                                                                                                                                                                                                                                                                                                          The invention relates to a method of identifying a zinc finger domain that recognises a target site on a DNA. The method comprises expressing hybrid nucleic acids with a test zinc finger domain in cells containing reporter construct, where the reporter gene is expressed above a given level when a transcription factor recognises a recruitment and a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc finger domain; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding zinc finger domain TG-ZFD-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-2001; 2001WO-KR00244
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 54; Page 69; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a zinc finger domain for e.g. designing new polypeptides that bind to a specific site on a DNA, comprises expressing hybrid nucleic acids with a test zinc finger domain in cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAU08558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2000; 2000KR-0007730
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 69
 BP;
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 A; 14 C; 18
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ger domain
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RESULT
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                                                                                                                          cc and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving c (II). (II) is useful for generating antibodies against it, detecting or c quantitating a polypeptide in tissue, as molecular weight markers and as c a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating c disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in c diagnostics, forensics, gene mapping, identification of mutations c responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and c amino acid sequences. AAS64197-AAS94564 represent novel human c diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                 Query Match
Best Local Similarity
 Matches
                                                                                Sequence 821
                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 4061; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2079 aggacacac 2087
                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding
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 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG04070.
 Conservative
                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel human diagnostic protein #4061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                  174 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder;
                 100.0%;
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                                                                                  234 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YT;
 0;
                 Score 49;
Pred. No.
                                                                                  215 G;
 Mismatches
                                                                                  198 T; 0
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                 .1e-13;
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                             Length 821;
 Indels
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caccagaggacacactcaggggagaagcc

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Query Match Best Local S Matches 29

Similarity

Conservative (

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1687

Score 29; DB Pred. No. 0.( 0; Mismatches

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Length 800; Indels

.00079;

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Gaps

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RESULT
                                                                                                cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
 Sequence 800 BP;
                                 present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                            cancer-associated nucleic acid molecules (N) and proteins (P), the proteins are collectively known as colon cancer antigens. \dot{}
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2813-2814; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                               AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer antigen encoding cDNA SEQ ID NO:888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-235357/24.
DB; AAG74401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US26524
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99US-0163280
 240 A; 173 C; 219 G; 166
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and/or treating colorectal cancers -
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 Ţ;
 2 other
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
 1645
               1659 caccagaggacacactcaggggagaagcc 1687
                                                                                                                                                                                      diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                      for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #26233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                        The polypeptide and polynucleotide sequences have applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 26233; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABG26242.
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food supplement; medical imaging; diagnostic; genetic d
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                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        oolynucleotides are also used in diagnostics as expressed sequence tags
                                                                             Local
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                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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caccagaggacacactcaggggagaagcc 167:
                                                              . Similarity
29; Conser
                                                                                                                                            2349 BP;
                                                               Conservative
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2000US-0649167
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                                                                                                                                            664 A;
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Pred. No.
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RESULT

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1659 caccagaggacacactcaggggagaagcc

Matches

Local

Similarity 29; Conserv

Conservative

0;

Mismatches

Score 29; Pred. No.

DB

Length 3582; Indels

0;

Gaps

0

.00078; 22;

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AAI58664
ID AAI5
21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                 system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, damemostatic and thrombolytic activity, cancer diagnosis and thrapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
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                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                        Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI58664 standard; cDNA; 3582
                                                                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - {\sf var}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200153312-A1
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Sequence
                          specification
                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAM39508
                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                            Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia; ss
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                                   disorders.
The sequence data
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Zhou P,
3582
                                                                                                                                                                                                                                                                            SEQ ID NO 867;
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2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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BP; 1024 A;
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Wehrman T, Xu C,
Goodrich R, Drmar
                                                                                                                                                                                                                                                                           10078pp; English.
                                        for this patent did not form part of the printed
826
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C;
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Drmanac R
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<u>ن</u>
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Xue AJ,
lac RT;
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Yang Y,
 1 other
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Zhang J;
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В

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caccagaggacacactcaggggagaagcc 1515

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RESULT 12
AA1604450/c
ID AA1604
XX AA1604
XX AA1604
XX AA1604
XX AA1604
XX Human;
XX Human;
XX Human;
XX Homo $
XX H
    Query Match
Best Local Similarity
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14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, hinhibin activity, chemotractic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids the encoded polypeptides (AAM38642-AAM42213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inflammation; chemotinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                             Sequence
                                                                                                                                          specification
                                                                                                                                                                                                             assays
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-442253/47.
                                                                                                                                                            The sequence
                                                                                                                                                                                      disorders
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                                                                                                                                                                                                           for receptor activity,
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Zhou P,
                                                                                               3582
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2000US-0553317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0653450.
2000US-0653191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 4439;
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Wehrman T,
                                                                                             821
                                                                                                                                                               data
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    1.0%;
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No.
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                                                                                                                                                                                                           inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAI57798-AAI61369) with nootropic,
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                         Length 3582;
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Zhang ,
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RESULT 13
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ID AALO022
XX AALO02
XX AALO02
XX Homan;
XX Human;
XX Human;
XX Homo s
PN W02001
XX Homo s
PN W0201
PN 01-AU
PR 11-AU
PR 11-SE
PR 01-SE
PR 01-SE
PR 01-SE
PR 06-SE
PR 06-SE
PR 06-SE
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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07-JUL-2000;
07-JUL-2000;
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14 - AUG -
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14-AUG-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human reproductive system related antigen cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL00216;
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                                                                                                                                                                                            2000US-0225270.
2000US-0225447.
2000US-0225757.
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2000US-0190076.
2000US-0198123.
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2000US-0184664.
2000US-0186350.
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                       2000US-0229509.
2000US-0229513.
2000US-0230437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
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                                                                                                                          2000US-0226868
2000US-0227182
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2000US-0220963
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2000US-0217496
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2000US-0216647
                                                         2000US-0229345
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                                                                                                      2000US-0228924
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08-NOV-2000
17-NOV-2000
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20-OCT-2000;
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20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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13-OCT-2000;
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14-SEP-2000

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29-SEP-2000

29-SEP-2000
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17-NOV-2000;
17-NOV-2000;
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02-OCT-2000;
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3-SEP-2000;
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2000US-0231243
2000US-02311414
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2000US-0231414
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2000US-0232981
2000US-0232399
2000US-02333063
2000US-02334997
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Matches 28
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
11-NOV-2000;
01-DEC-2000;
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06-DEC-2000;
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P-PSDB;
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                                                                                                                                     cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fingicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the prevention including cancer. invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen
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                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding a novel secreted protein, Seq
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DB; AAM94246.
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                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100.0%; 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
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2000US-025198
2000US-0256719
2000US-0251479
2000US-0251856
2000US-0251869
2000US-0251869
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2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249299.
2000US-0249300.
2000US-0250160.
2000US-0250391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reproductive system related antigens. These can lon and treatment of reproductive system disorders {\bf r}. The present sequence is a coding sequence of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 217; 1297pp + Sequence Listing; English
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Pred. No. 0.0
0; Mismatches
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0.0025;
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14-AUG-2000

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23-AUG-2000

201-SEP-2000

21-SEP-2000

21-SEP-2000
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07-JUN-2000,
28-JUN-2000,
30-JUN-2000,
07-JUL-2000,
07-JUL-2000,
11-JUL-2000,
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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14 - AUG
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14-JUL-
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-MAR-2000;
-APR-2000;
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2000US-0179065
2000US-0180628
2000US-0180628
2000US-0180628
2000US-0189874
2000US-0199123
2000US-0199123
2000US-0199123
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2000US-0233484
2000US-0233844
2000US-0233844
2000US-0233834
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 29-SEP 2000
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02-OCT 2000
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03-OCT 2000
03-OCT 2000
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09-NOV 2000
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01-DEC 2000
 WPI;
                            Rosen
 2001-488783/53
                          CA,
                                                          HUMAN
                          Barash SC,
                                                                                  2000US-0236368
2000US-0236369
2000US-0236802
2000US-0236802
2000US-0236802
2000US-0237039
2000US-0237039
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2000US-0249216
2000US-02511868
2000US-02511868
2000US-02511868
2000US-02511899
2000US-0251989
                                                        GENOME
                                                          SCI
                             Ruben
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AAS26635
ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC encoded secreted proteins. The nucleic acids and proteins are used to cc prevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They cc are also used in diagnosing a pathological condition or susceptibility ct to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in cc diagnostic immunoassays e.g. radioimmunoassays or enzyme linked c include autoimmune diseases e.g. neoplasms of the breast or liver, cc cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. rheumatoid arthritis, cerebral ischaemia, angiogenesis, nervous system disorders e.g. cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders caused by bacteria, viruses and fungical conditionator of sisted in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to crepture takin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2149 tcatcagacaccagaggacacacacag 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                          cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation;
 31-JAN-2000; 2000US-0179065
04-FEB-2000; 2000US-0180628
24-FEB-2000; 2000US-0184664
                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                               cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                  17-JAN-2001;
                                                                                                                                                                                                 skin
                                                                                                                                                                                                                                                             neuroprotective; antibacterial; virucide; fungicide; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                            Human; immunosuppressive; antiarthritic; ds; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                              Human genomic DNA encoding partial novel secreted protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS26635 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 27; Conserv
                                                                                                                                                                                              ageing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 128;
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                  2001WO-US01341
                                                                                                                                                                                                 food
                                                                                                                                                                                                additive; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; 1
0.0077;
hes 0;
                                                                                                                                                                                                antiproliferative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indels
                                                                                                                                                                                                                                                                                                             nootropic;
                                                                                                                                                                                                                                                                                             opthalmalogical;
                                                                                                                                                                                                                                                               cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                              Seq ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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   18 - SEP - 2000
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25 - SEP - 2000
27 - SEP - 2000
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02 - CCT - 2000
02 - CCT - 2000
02 - CCT - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

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05-SEP-2000

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06-SEP-2000
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14-AUG-2000;
14-AUG-2000;
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2000US-0189874.
2000US-0190076.
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2000US-0225757.
2000US-0225758.
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2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
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2000US-0229513.
2000US-0230437.
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2000US-0226279
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2000US-0232399
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2000US-0231243
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2000US-0216647
                                2000US-0236802
2000US-0237037
                                                                2000US-0236369
2000US-0236370
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ID XXX ACC XXX

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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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20-CCT-2000
20-CCT-2000
01-NOV-2000
08-NOV-2000
09-NOV-2000
09-NOV
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20-OCT-2000;
20-OCT-2000;
                                             New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000;
                                                                                                                                                                                                (HUMA-)
                                                                                                                                                                                              HUMAN GENOME
                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                 2000US-0241785

2000US-0241786

2000US-0241808

2000US-0241808

2000US-0241826

2000US-0246474

2000US-0246475

2000US-0246476

2000US-0246524

2000US-0246526

2000US-0246526

2000US-0246526

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2000US-0246611

2000US-0249207

2000US-0249207

2000US-0249217

2000US-0249217

2000US-0249217

2000US-0249214

2000US-0249216

2000US-0251030

2000US-0251030

2000US-02511868

2000US-0251869

2000US-0251899

2000US-0251899

2000US-0251989

2000US-0251989

2000US-0251989
                                                                                                                                                                                                SCI INC
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Disclosure; SEQ ID No 1609; 980pp; English

and

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AAV64361
ID AAV6
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease, infections caused by bacteria, viruses and fun and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inmunosorbant assays (ELISA). Disorders which are diagnosed or Lieuwinclude autoimmune diseases e.g. rheumatoid arthritis, include autoimmune diseases e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebral ischaemia, angiogenesis, nervous system disorders e.g. cerebral ischaemia infections caused by bacteria, viruses and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoasorbant assays (BLISA). Disorders which are diagnosed or treated inmunoasorbant assays (BLISA). Disorders which are diagnosed or treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2149 tcatcagacaccagaggacacacacag 2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence is a genomic DNA encoding a partial novel secreted protein the invention.
                              New polynucleotides encoding stem cell zinc fingers - useful fi
                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SZF1-2; human; stem cell zinc finger; transcription factor; haematopoiesis; CD34+; gene therapy; ss.
              proteins
                                                                                    P-PSDB; AAW81632.
                                                                                                   WPI; 1999-009328/01.
                                                                                                                                     Civin CI,
                                                                                                                                                                                                        08-APR-1997;
                                                                                                                                                                                                                                          08-APR-1998;
                                                                                                                                                                                                                                                                            15-OCT-1998
                                                                                                                                                                                                                                                                                                             WO9845326-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human stem cell zinc finger SZF1-2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV64361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV64361 standard; cDNA; 3099
                                                                                                                                                                     (OSIR-) OSIRIS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962 tcatcagacaccagaggacacacacag 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
27; Conserv
                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                          97US-0041811
                                                                                                                                                                                                                                          98WO-US06925
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 379..1465
                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                       INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   в 22;
.0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2717;
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                                                  useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
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Disclosure; Page 44-46; 76pp; English.

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RESULT 17
ABL00474/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          concentrations of SZF1-2 can cause haematopoletic cells to differentiations of SZF1-2 can cause haematopoletic cells to differentiation of szF1 was made through the random sequencing of a continuous of several hundred clones from a cDNA library prepared from thuman bone marrow CD34+ cells. One of the fragments was unique but showed homology to the Kruppel family of zinc finger proteins. This fragment was used to screen cDNA libraries from CD34+ cells, C K562 cells and human lung. Overlapping cDNA fragments which hybridised to the probe gave rise to 2 alternatively spliced cDNA products, termed SZF1-1 (see AAV64360) and SZF1-2. The gene is found on chromosome 3. Database searches showed the most highly related genes to be ZN133, K1d1 and ZNF95 (658, 55% and 45% homology at the nucleotide level, respectively). The invention additionally provides recombinant vectors and host cells, and a method of producing SZF1 polypeptides. The polynucleotides may be utilised for gene therapy in a host to replace or supplement a celective SZF1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27; Conserv
                            polymorphisms, pathology, e.g. sequence polymo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1913 tcatcagacaccagaggacacacacag 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL00474 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA sequence includes a coding region for human stem cell zinc finger protein SZF1-2 (see AAW81632), a novel transcription factor that appears to be expressed in most cell types and tissues and which may be involved in the maturation of CD34+ cells; certain
                                                                                                                                                                                                                                                                                                                                                                                          Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                           Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a
                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                              24-NOV-1999;
                                                                                                                                                                                                                                              22-NOV-2000; 2000WO-US32311.
                                                                                                                                                                                                                                                                              31-MAY-2001
                                                                                                                                                                                                                                                                                                              WO200138586-A2
                                                                                                                                                                                                                                                                                                                                                                            infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human silent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-2002
                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcatcagacaccagaggacacacacag
                                                                                                               2001-355949/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3099
                              polymorphism
                                                                                                                                                                                                                                                                                                                                                                            polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          noncoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B₽;
                                                                                                                                               Leach
                                                                                                                                                                                                              99US-0167383.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%;
                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP oligonucleotide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
0.0076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Claim 1; Page 388; 674pp; English

ABL00010 to ABL01104 represent human nucleic acid oligonucleotides comprising one or more single nucleotide polymorphisms (SNPs). ABB56 to ABB5603 represent human peptides encoded by some of the SNP oligonucleotides. The sequences from the present invention can have

ABB56531

cytostatic, antiinflammatory, neuroprotective and

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RESULT 18
ABL00878/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 to ABB56903 represent human peptides encoded by some of the SNP oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a subject suffering from, at risk for, or suspected of, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised polymorphic protein (e.g., for use in measuring levels of the polymorphic protein (e.g., for use in measuring levels of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1378 gctttagccagaagtcacacctcat 1402
                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic protein (e.g., for use in measuring level polymorphic protein within appropriate physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
                                                                                                                                Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a
                                                                                                                                                                                                                                                                                                                                               31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single nucleotide polymorphism;
immunosuppressive; antiinflammatory; no
autoimmune disease; inflammation; cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL00878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL00878 standard;
                                                                                       Claim
                                                                                                                                                                                                                           Shimkets RA, Leach
                                                                                                                                                                                                                                                                                     24-NOV-1999;
                                                                                                                                                                                                                                                                                                                 22-NOV-2000; 2000WO-US32311
                                                                                                                                                                                                                                                                                                                                                                             WO200138586-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; polymorphic protein; ds.
                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                             2001-355949/37.
                                                                                       ۳.
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                                                                                      Page 509;
                                                                                                                    polymorphism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 9 A; 10 C;
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                                                                                      674pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n; SNP; polymorphism; cytostatic;
neuroprotective; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
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RESULT :
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Best Local
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11-JAN-2000;
02-MAY-2000;
                        molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed consistent with the construction of the sequence of the sequence of the sequence of the sequence data for this patent did not form part of the printed consistent with the sequence of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).
specification,
                                                                                                                                                                                                                                                                                                                                                                                                     clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to primers for synthesising full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use in genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                        clones. 830 cDNA molecules encoding a humisolated and nucleotide sequences of 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
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su A, Sugiyama
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; 2000JP-0118774.
; 2000JP-0183765.
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    but was obtained in CD-ROM format directly from EPO
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100.0%; Pr
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a T, Nagai
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K, Kojima
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                                                                                                                                                                                                                                                                                                                                                        human protein have been 
'- and 3'-ends of the cDNA
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T, Koga
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                           clones. 830 cDNA molecules encoding a human protein have been solated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                           Sequence
                                                                                                                 representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                             The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been
                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                 Example 11; SEQ ID NO 2271; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                     830 Primers useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu
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Nagai K, Kojima
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ruman neuroblastoma. The primer in diagnosing the susceptibility indicators
                                      Human; cytokine; cell proliferation; cell differentiation; growth f haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-565584/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI95339;
                                                                                                                                                                         Human PRO1847
                                                                                                                                                                                                                                                                                                              ABA08823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids originating useful as probe or primer neuroblastoma, malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2001; 2001WO-JP01629
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  atherosclerosis;
                                                                                                                                                                                                                    11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                  ABA08823;
                                                                                                                                                                                                                                                                                                                                                                                                                           368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-cancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                       acacacaggagagaagccttatg
                                                                                                                                                                                                                                                                                                                                                                                                                                              acacacacaggagagaagccttatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         information for diagnosing prognosis is related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroblastoma expressed polynucleotide SEQ ID NO 1414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIBA PREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                      inflammatory condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for N-myc and TrkA genes
                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1061; 2979pp;
                                                                                                                                                                       homologue-encoding cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nosing the prognosis of human neuroblastoma, malignancy an indicators or tumour markers for anti-cancer agents. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
tory condition; proliferative retinopathy coronary heart disease; arterial ischaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARM
                                                                                                                                                                                                                                                                                                              cDNA;
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                                                                                                                                                                                                                                                                                                              871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene expressed in human neuroblastoma, in diagnosing prognosis of human and susceptibility indicator or tumour marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred.
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No.
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                                                                                                                                                                         SEQ ID NO:599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 814;
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                                                                                                                                factor;
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healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders, polypeptides with growth factor activity may be used in cell cultures promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleoti may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention method we various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000;
27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 600; 1963pp; English.
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2000US-0560875
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Matches 25
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Matches 25; Conserv
                                                                                                                                   The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
AAK91560 standard;
                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                               11-JAN-2000;
Q2-MAY-2000;
                                                                                                                      Sequence 2200
                                                                                                                                                                                                                                                                           830 Primers useful for synthesizing
                                                                                                                                                                                                                                                                                              P-PSDB; AAM93641.
                                                                                                                                                                                                                                                                                                                    Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK94575 standard; cDNA; 2200
                                                                                                                                                                                                                                                                                                                                              (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK94575;
                                           343
                                                           224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 ggatgtggctgtgtacttcacccag 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                  ggatgtggctgtgtacttcacccag 248
                                                                                                                                                                                                                                                                                                    2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggatgtggctgtgtacttcacccag
                                          ggatgtggctgtgtacttcacccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length
                                                                                                                                                                                                                                                                    genetic manipulation
                                                                             Similarity 25; Conser
                                                                                                                                                                                                                                                                                                                             Nishikawa T,
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                  ID NO 3494; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                               2000JP-0118774
2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                99JP-0194486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA,
                                                                                                                      579 A; 558 C; 529
CDNA; 688
                                                                                    0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                            Isogai T,
                                                                                                                                                                                                                                                                                                                     η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                    Nagai
                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                    Score 25;
Pred. No.
ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO: 3494.
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                    Hayashi K,
K, Kojima
                                                                                                                      ი
ც
                                                                                                                                                                                                                                                                            full length cDNA clones
                                                                                                                      534 T; 0 other;
                                                                                    DB 22;
0.074;
                                                                                                                                                                                                                                                                                                                  Ishii S,
                                                                            0
                                                                                                                                                                                                                                                                                                                     Otsuki
                                                                                            Length 2200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                    Kawai
T, Ko
                                                                                                                                                                                                                                                                                                                    Koga
                                                                            0,
                                                                                                                                                                                                                                                                            and their
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                                                                            Gaps
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PN XXX XXX AXX
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                                                                                                                      RESULT
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Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
Homo sapiens
                                               Human;
                                                                                           Human cDNA clone representative sequence, SEQ ID NO:
                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                        AAK93129 standard;
                                                                                                                                                                                            AAK93129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 688 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to primers for synthesising full length clones. 830 cDNA molecules encoding a human protein have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA 5'-end sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ciones. 830 cDNA molecules encoding a human protein have been solated and nucleotide sequences of 5', and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK91560;
                                                                                                                                                                                                                                                                                                                                                                                   214 tggcattcagggatgtggctgtg 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 0.8%; S. Local Similarity 100.0%; les 23; Conservative 0;
                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                        tggcattcagggatgtggctgtg 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                            full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nishikawa T, I
su A, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 20; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 A; 146 C; 173 G;
                                            cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                      CDNA; 688
                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Hayashi K,
a T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 22;
Pred. No. 0.72;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hii S, Kawai Y;
Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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QΥ
   RESULT 26
ABA50438/c
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Best Local S
Matches 23
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the nomology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2001
                                                                          30-JAN-2001;
                                                                                                  09-AUG-2001
                                                                                                                                                  Homo sapiens
                                                                                                                                                                           disease;
                                                                                                                                                                                                                                       01-FEB-2002
                                                                                                                                                                                                                                                                ABA50438;
                                                                                                                                                                                                                                                                                         ABA50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; SEQ ID NO 1589; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELI-) HELIX RES INST
                                                                                                                         WO200157271-A2
                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                               Human breast cell single exon nucleic acid probe #9133
                                                                                                                                                                                                                                                                                                                                                                 214 tggcattcagggatgtggctgtg
                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; es 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primers useful for synthesizing full length cDNA clones and in genetic manipulation \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                     tggcattcagggatgtggctgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 cDNA molecules encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889
                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                         standard;
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0194486.
2000JP-0118774.
2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 156 A; 146 C; 173 G;
                                                                                                                                                                                                                                       (first entry)
                                                                          2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama
                                                                                                                                                                           SS
                                                                                                                                                                                                                                                                                        DNA; 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T,
a T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                       383
                                                                                                                                                                                                                                                                                                                                                                              236
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi K, I
K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human protein have been
5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22
0.72;
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                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 688
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koga
                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                  Query Match
Best Local S
                                       Matches
                                                                                                                                                         determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less blas than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                        nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
04-OCT-2000;
                                                                                                                           Sequence 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spatially-addressable set of single exon nucleic acid post ful for measuring gene expression in sample derived from ast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                     .larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 9133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236359.
2000GB-0024263.
                                                                                                                           B₽;
                                                                                                                           258 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a spatially-addressable set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                        0.8%;
                                                                                                                         462 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327pp + sequence listing; English
                                     0;
                                                    Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR
                                                                                                                             386
                                       Mismatches
                                                                                                                         G;
                                                                                                                             406
                                                      DB 22
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon nucleic acid probes, sample derived from human
                                                                       22;
                                                                                                                             T; 0 other;
                                       0
                                                                       Length 1512;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of single
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В
  ABA68388/c
                                                                                                                                                                                                                                        RESULT
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                            1490 acaccagaggacacactcagggg 1512
                                                                                                                                              Human;
                                                                                                                                                              Human foetal liver single exon nucleic acid probe #16693
                                                                                                                                                                                01-FEB-2002
                                                                                                                                                                                                   ABA68388;
                                                                                                                                                                                                                    ABA68388 standard; DNA; 1512
                                                                                                           WO200157277-A2
                                                                       30-JAN-2001;
                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                  983 ACACCAGAGGACACACTCAGGGG
                                                                                                                                              foetal liver; gene expression;
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                       2001WO-US00669
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                   961
                                                                                                                                             single exon nucleic acid probe;
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ο<sub>γ</sub>
RESULT 28
ABA35;382/c
ID ABA35382 standard;
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Best Local
                                                                                                                        26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1490
                   Single
                                      WPI; 2001-488899/53
                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                              WO200157274-A2
                                                                                                                                                                                                                                                                                Human; gene expression; heart; microal cardiovascular disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                              27-SEP-2000;
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                      congenital heart disease;
                                                                                                                                                                                                                                                                                                               Probe
                                                                                                                                                                                                                                                                                                                                   23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                        ABA35382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1512 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                            983 ACACCAGAGGACACACTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        acaccagaggacacactcagggg
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                                                                                                                                                                                                                                                                                                               #13848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                   exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                            Hanzel
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                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0609408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                      2001WO-US00666
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                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 16693; 639pp +
                                                            R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DK,
                                                                                                                                                                                                                                                                                                            gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 A; 462 C; 386 G;
                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%;
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                                                                                                                                                                                                                                                                                          heart; microarray;
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                  probes
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                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR;
                  analyzing gene expression
                                                            DR.
                                                                                                                                                                                                                                                                                cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            did not form part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .71;
                                                                                                                                                                                                                                                                                           vascular system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,:
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RESULT 2
AAK16761/
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Best Local S
Matches 23
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26-MAY-2000;
30-JUN-2000;
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04-OCT-2000;
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AAK16761 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                              Single
                                                                                                                   WPI; 2001-483446/52
                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                               epilepsy;
                                                                                                                                                                                                                                                                                                                                                                         microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK16761;
                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                         30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1512 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes measuring human gene expression in a sample derived from human he present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4;
                                                                                                                                                                                                                                                                                                                    WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             983 ACACCAGAGGACACACTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                              exon nucleic acid
                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                               cancer;
                                                                                                                                          Hanzel
                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                          2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                          DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                              probes
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Pred. No.
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                                                                                                                                          Rank DR;
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                                                                                              for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 G;
                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                        probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 T; 0 other;
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0.71;
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                                                                                              expression in
                                                                                                                                                                                                                                                                                                                                                                                                         16752
                                                                                                                                                                                                                                                                                                                                                                          schizophrenia;
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heart.
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                                                                                               human
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system

SEQ

ID NO:

16752;

650pp + Sequence

Listing;

English

y enable the diagnosis such as Alzheimer's d

cancers.

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RESULT 30
AAK42537/c
ID AAK425
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                                      Matches
                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
-30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1490
                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                               WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; cancer; leukaemia; lymphoma; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
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         1490 acaccagaggacacactcagggg 1512
                                                                                                                                                                             Example 4; SEQ ID NO: 17094; 658pp + Sequence Listing; English
                                                                                                                                                                                                 analyzing
                                                                                                                                                                                                           Human
                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                           04-OCT-2000
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy and invention.
                                                                                     Sequence 1512
                                                                                                                                                                                                                                                                      (MOLE-)
983
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                                                                                                                                                                                                                              2001-488900/53.
ACACCAGAGGACACACTCAGGGG 961
                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for
zing gene expression in human bone marrow -
                                                Similarity
                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-023659.
2000US-023659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                marrow
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                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258
                                                                                      258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed exon; gene expression analysis; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                  0.8%; 5cc
100.0%; Pr
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                                                                                     Α,
                                                                                                                                                                                                                                                  Chen W,
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                                                                                     462 C;
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                                                                                                                                                                                                                                                                       INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                     Score 23; DB; Pred. No. 0.7
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Pred. No.
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                                                                                      386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
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                                                                                      G;
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0.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe
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                                     0,
                                                       Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO: 17094.
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                                      Indels
                                                                                                                  treatment of cancers sequence is one of
                                      0,
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                                     Gaps
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RESULT 31
AA123284/C
ID AA1232
AC AA1232
AC AA1232
AC AA1232
XX Probe:
XX Probe:
XX Probe:
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RESULT 32
AA148604/c
ID AA1486
XX
AA2 AA1486
XX
DT 17-OCT
XX
DE Probe
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid analyzing gene expression in human cervical ep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #13217
                                                     17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1512 BP; 258 A; 462 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID No 13217; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00670
                                                                                                      AAI48604;
                                                                                                                                                      AAI48604 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                                                                                                                                                                                                                    983 ACACCAGAGGACACACTCAGGGG 961
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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); 2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                0.8%;
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                                                                                                                                                           ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB
0.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical epithelial cell;
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epithelial cells
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В Ş

Probe #17290 used

to measure gene expression

in human

placenta sample

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RESULT 33
AAI08925/c
ID AAI08925;
XX
AC AAI08925;
XX
DT 09-OCT-2001 (first |
DT 09-OCB #8916 used to |
XX
DE Probe #8916 used to |
XX
Probe; human; breast
XX
Probe; human; breast
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Probe; human; breast
XX
PROBO Saplens.
XX
PN W0200157270-A2.
XX
PD 09-AUG-2001.
XX
PP 09-AUG-2001; 2001WO-XX
PF 29-JAN-2000; 2000US-PR 26-MAY-2000; 2000US-PR 30-JUN-2000; 2000US-PR 30-J
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Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probe. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes a for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                            Probe; human; breast
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zing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microarray;
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     ; 2000US-0180312.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                       2001WO-US00661
                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                          to measure
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                                                                                                                                                                                                                          disease; breast cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 C;
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                                                                                                                                                                                                           breast
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                                                                                                                                                                                                           disease;
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                                                                                                                                                                                                                         development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                           non-carcinoma
                                                                                                                                                                                                                            disorder;
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RESULT 3
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Matches 23
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                    08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast,
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                                                                  Ota T,
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                                                                                                                                                                                                                                                                                                                   05-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK94635;
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2001-524255/58
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human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full length cDNA;
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                                         Nishikawa T,
su A, Sugiya
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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                                           Sugiyama
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                                         Isogai T,
wa T, Nagai
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                                           Hayashi K,
K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0
                                           Ishii S,
S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
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                                              Kawai
T, Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS
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                                                                  ۲;
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                                              Ξ
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δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA molecules have been determined. Primers for synthesising the full lengchare useful for clarifying the function of the protein encoded by cDNA are useful length clones were obtained by construction of full the cDNA. The full length clones were obtained by construction of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830
use
                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuman breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA45305;
 The invention relates to nucleic acid probes for \boldsymbol{\pi}
                                           Claim 1;
                                                                                    New spatially-addressable set of single exon nucleic acid probes useful for measuring gene expression in sample derived from human
                                                                                                                                                                                                                27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                     26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                 WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA45305 standard; DNA; 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1623 BP; 389 A; 346 C; 376 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                            21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 tggcattcagggatgtggctgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 tggcattcagggatgtggctgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primers useful for synthesizing full length cDNA clones and their in genetic manipulation - \,
                                                                                                                             2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
23; Conser
                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                      comprises number of single exon nucleic acid
                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                              2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234369
2000US-0236359
2000US-0236359
2000US-0236353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                          ID NO 4000; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                         Chen W,
 measuring
             a spatially-addressable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB
s; Pred. No. 0.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probe #4000
                                                                                                                                                         Rank
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  512 T; 0
 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
 set of on in a s
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                                                                      probes
 sample
             single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
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RESULT 36
ABA55794/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids controlled from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for controlled from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for controlled from the expression of regions of genomic DNA predicted to controlled from the expression analysis is useful for gene discovery, and for determining predisposition analysis for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater controlled from the expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this pattent did not form part of the controlled specification, but was obtained in electronic format directly controlled from wife at the wife of the invention in the probabilished controlled probabilished controlled from the invention.
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA55794 standard; DNA; 1965
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                                                                                                                               Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA55794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1965 BP;
                                                                                                 Claim 1;
                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                    2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
23; Conserv
                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS
                                                                                                 SEQ ID NO 4099; 639pp + sequence listing; English
                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 A;
                                                                                                                                                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23;
Pred. No.
                                                                                                                                                                                                                     Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 G; 518 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #4099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
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measuring and fetal liver.

displaying gene expression The present sequence is a si

in samples derived from

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RESULT 37
ABA25474/c
ID ABA25474 standard; DNA; 1965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 23
                                          present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in sample derived from human heart. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, the monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                 Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                         Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe of the invention. Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1490 acaccagaggacacactcagggg 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
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                                                                                                                                                                                                                                                                                                (MOLE-)
                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
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                                                                                                                                                                                                                                                  2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #3940
                                                                                                                                                                                                                         exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                       ; 2000US-0180312
2000US-0207456;
2000US-0608408;
2000US-0632366;
2000US-0234687;
2000US-0236359;
2000US-0236359;
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                                     ID No
                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                          DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 A; 584 C;
                                                                                                                                                                                     3940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression analysis in human heart cell
                                                                                                                                                                                  530pp; English.
                                                                                                                                                                                                                         probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss.
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                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497
                                                                                                                                                                                                                        for analyzing
                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
0.71;
                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1965;
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                                                                                                                                                                                                                        expression
                                  part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          part of the format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sample
                                                                                                                                                                                                                         'n
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BP;

366

Α, 584

c;

497

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518

Η.

0 other;

RESULT 39 AAK29501/c

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AAKO4015/c
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                 δÃ
                                                                                В
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                                   Query Match
Best Local S
Matches 23
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Best Local S
Matches 23
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26-MAY-2000; 2000US-0608408.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
04-OCT-2000; 2000GB-0024263.
1110 ACACCAGAGGACACTCAGGGG 1088
                  1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1490
                                                                               Sequence 1965
                                                                                                          brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; genumicroarray; Alzheimer's disease; epilepsy; cancer; ss.
                                                                                                         epilepsy and cancers.
                                                                                                                                              The present invention provides probes which are derived from c
                                                                                                                                                                                                    Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK04015 standard;
                                                                                                                                                                         Example 4; SEQ
                                                                                                                                                                                           brains
                                                                                                                                                                                                                                       Penn
                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                     WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK04015;
                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acaccagaggacacactcagggg
         SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain
                                                                                                                                                                                                  exon
                                    Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
23; Conser
                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS
                                                                                                                                                                                                                                      Hanzel
                                   0.8%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                 2001WO-US00667
                                                                                BP;
                                                                                                                                                                         ID NO:
                                                                                                                                                                                                                                       DK,
                                                                                366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%;
                                                                                A; 584 C;
                                                                                                                                                                         4006; 650pp + Sequence Listing;
                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                            ovides a number of single exon nucleic from genomic sequences expressed in the
                                                                                                                                                                                                   probes
                                                                                                                                                                                                                                       ξ
                                   0;
                                   Score 23; DB
Pred. No. 0.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                  1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression analysis; probe;
ase; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                       Rank
                                                                                497
                                                                                                                                                                                                  for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                           . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe
                                                                                ç;
                                                                                                                                                                                                                                        DR
                                                                                518
                                           DB 22
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                       analysis;
                                                                                0
                                    0,
                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ:
                                                                                                                                              expressed in the human
                                                                                other;
                                                    Length 1965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                   expression
                                                                                                                                                                         English
                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                    ä
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                     samples
                                                                                                                                                                                                    human
                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 40
AAI14072/c
ID AAI140
AC AAI140
AC AAI140
AC AAI140
XX
DT 12-OCT
XX
XX
Probe
XX
Probe;
KW Probe;
KW Probe;
XX
OS Homo s
XX
PN WO2001
                                                                                                                                                                                                                              QY
                                                                                                                                                                                    Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                    1490
                                                                                                                                                    1110 ACACCAGAGGACACACTCAGGGG
                                                                                                                                                                                                                              Sequence 1965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                           AAI14072 standard;
                                                                                                                                                                                                                                                                                                       Example 4;
                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK29501 standard;
                  Homo sapiens
                                  cervical cancer;
                                         Probe; human; microarray;
                                                                           12-OCT-2001
                                                                                          AAI14072;
                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                2001-488900/53
                                                                                                                                                             acaccagaggacacactcagggg
                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                      genome-derived single exon nucleic acid probes useful for zing gene expression in human bone marrow \boldsymbol{\cdot}
                                                         #4005
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                              of the invention
                                                                                                                                                                                                                                                                                                      SEQ ID NO: 4058; 658pp + Sequence Listing; English
                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00668
                                                         gene
                                  SS.
                                                                                                                                                                                                                             366 A; 584 C; 497 G;
                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 1965
                                                                                                                                                                                            0.8%;
                                                         expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                            1965
                                         gene
                                                                                                                                                                                     0,
                                                                                                                                                                                    Score 23; DB; pred. No. 0.7
                                                                                                                                                    1088
                                                                                                                                                                    1512
                                                                                                           ВP
                                         expression;
                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                             518 T; 0 other;
                                                                                                                                                                                             0.71;
                                                                                                                                                                                                     22;
                                         cervical epithelial cell;
                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:
                                                                                                                                                                                                    Length 1965;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4058
                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                      of cancers
is one of
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     0;
                                                                                                                                                                                                    RESULT 4
AAI35452/
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Query Match
Best Local S
Matches 23
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26-MAY-2000;
30-JUN-2000;
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                                                                                                                                                                                                                                                                 genetic
                                                                                                                                                                                                                                                                                                                                                                                                  AAI35452;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI35452 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                      Probe #4138 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                         WO200157272-A2
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                   Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001
                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
23; Conserv
                                                                                                                                                                                                                                                                   disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 4005; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US00670
                                                                                                                 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 A; 584 C;
                                                                                                                                                                                                                                                                                   human; placenta; antenatal diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT 42
AAI03925/c
ID AAI039
  ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                            04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probe. The present sequence is one such probe. The probes are useful fit producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes a for antenatal diagnosis of human genetic disorders.
                                            Novel
                                                                                                                                                                                                                                                                                                                                                                                       1110 ACACCAGAGGACACTCAGGGG 1088
                                                                                                                                                                                                                                                                                                                                                                                                 1490 acaccagaggacacactcagggg 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
04-OCT-2000;
                   Claim
                                                                                                                   04 -OCT
                                                                                                                                                                                         29-JAN-2001;
                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                            WO200157270-A2
                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer;
                                                                                                                                                                                                                                                                                          Probe
                                                                                                                                                                                                                                                                                                           09-OCT-2001
                                                                                                                                                                                                                                                                                                                            AAI03925;
                                                                                                                                                                                                                                                                                                                                             AAI03925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                              intlammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1965 BP;
                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                SG,
                                                               2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-488897/53
                   25;
                                    single exon nucleic human breast -
                                                                                                                                                                                                                                                                                         #3916 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic ac
zing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                  MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                             standard;
                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID No 4138; 654pp; English.
                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                              disease; proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                         2001WO-US00661
                                                                                                                  2000GB-0024263
                  ID No 3916;
                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
                                                                                                                                                                                                                                                                                                                                             DNA; 1965
                                                                                                                                                                                                                                                                                        measure
                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 C;
                 322pp;
                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23;
Pred. No.
                                            probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
novel single
                  English.
                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR
                                                                                                                                                                                                                                                              breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22
0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid
                                             ť
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                        in human
                                            measuring
                                                                                                                                                                                                                                                                       development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
exon
                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The probes are useful
                                                                                                                                                                                                                                                                                         breast
                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes
                                             expression
                                                                                                                                                                                                                                                                                        sample
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
probes
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SENP)
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are more.
                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypmerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for the polynucleotides are also used in diagnostics as expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1490 acaccagaggacacactcagggg 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, undiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to biodiversity.
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P-PSDB; ABG16854.
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23-AUG-2000;
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                                                                                                                                                                    Claim
                                                                                                                                                                                                biodiversity
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23; Conserv
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                                                                                                                                                                    SEQ ID No
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Matches
polynucleotides. The library is used to detect unitarity and can genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams LT,
Reinhard C, F
Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from Westerficiation, but was obtained in electronic format directly from Westerficial that the absolute of the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                Library of polynucleotides for diagnosing a cancerous state mammalian cell and detecting cancer, particularly of the col prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kita
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                                                                                                                                                                                                                                                                                                                                          Page 1017; 1046pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garcia
                                                                                                                                                                                                                                              sequence is one of 3351 sequences in a library of human ides. The library is used to detect differentially expressed
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Pot D, Lamson (
Labat I, Leshk
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amson G, Drn
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Query Match Best Local S Matches 22

22; Similarity

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dysplasia
                                                                                                            The present sequence is given in a specification relating to compound for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer, especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lung tumour-specific cDNA #187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1999;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-1999;
09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060077-A2
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Sequence 484
                                                                                  especially lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtggctgtgtacttcacccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour protein; lung cancer; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-638466/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtggctgtgtacttcacccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor polypeptides and monitoring or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0518809
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    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0285323.
99US-0370838.
99US-0476235.
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                                                                                       cancer.
    145 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA; 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mohamath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.8%;
    106 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽,
    135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides, useful cancer, especially lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secrist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
No.
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        98
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    Τ,
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        0
                                                                                                                 xpressing the polypeptides ncer. The polypeptides are progression of cancer,
    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                  compounds
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                                                                                                                                                    Query Match
Best Local S
Matches 22
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05-JUN-2000;
18-AUG-2000;
                                                                                                                               1089
                                                                                                                                                                                                                           The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is human lung tumour-specific cDNA.
            07-NOV-2001
                                                                                                                                                                                                        Sequence 484
                                                                                                                                                                                                                                                                                                                                                           diagnosis
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14-DEC-2000;
                                 AAS26521;
                                                     AAS26521 standard;
                                                                                                                                                                                                                                                                                                                                      Example 4; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lung
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                                                                                                                                                   . Similarity 100 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ, P
RA, Fling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 484
                                                                                                                                                                                                                                                                                                                                                          lung-specific polynucleotides
and treatment of disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour-specific 2LT-120 cDNA
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; 2000US-0588937.
; 2000US-0640878.
; 2000US-2345179.
; 2000US-0704512.
; 2000US-0738973.
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                                                                                                                                                                                                        BP;
           (first entry)
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                                                                                                                                                                                                                                                                                                                                     256-257; 378pp; English.
                                                                                                                                                                                                        145
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                                                     cDNA;
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SP, Algate
                                                                                                                                                              .0%;
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immune response;
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Pred. No
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                                                                                                                                                    Mismatches
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PA, Elliot
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2.2
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                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                          polypeptides
g cancer -
                                                                                                                                                                                                        0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; ; lung cancer;
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14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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07-JUN-2000;
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04-FEB-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                    14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide;
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2000US-0225758.
2000US-0225759.
2000US-0226279.
2000US-0226681.
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opthalmalogical;
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KW Huma
KW Limmu
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Human 23-JAN-2002 ABA21456; ABA21456

nervous

system

related polynucleotide SEQ ID NO 13787.

(first entry)

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;

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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                        rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. and fungi
                                                                                                                    and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
                                                                     sequence
                                                                                     capabilities, fat content, lipid, protein, carbohydrate, vitamins minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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P-PSDB; AAU16534.
                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent, treat or ameliorate a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded
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 Similarity 100.0%; 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted
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                                                                     encodes
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2000US-0251868.

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2000US-0254097.
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                                                                     a novel secreted protein of
                                      0.8%;
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Score 22; DB; Pred. No. 2.2
0; Mismatches
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                                Length 758;
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                                                                     invention
                                                                                                                                          used
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Homo sapiens W0200159063-J 16-AUG-2001 17-JAN-2001 24-FEB-2000 24-FEB-2000 16-MAR-2000 17-MAR-2000 17-MAR-2000 11-MAR-2000 11-MAR-2000 11-JUL-2000 07-JUL-2000 07-JUL-2000 11-JUL-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-AUG-2000 11-SEP-2000 01-SEP-2000
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18-APR-2000;
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Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's is a service of the adrenal services of the adrenal services of the adrenal gland, bone bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's interestinal tract, lung, or urogenital services mellitus de la concentract de la concentract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for preventing, cancers and metastases
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                                                                                                                                                                                                                                                                                                     WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel (ABB14678-ABB18001) useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 13787; 1701pp + Sequence Listing; English
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22; Conserv
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2000US-0179065.
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                                                                                                                                                                                                       2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                               haematopoietic; immune/haematopoietic antigen; cancer; ne therapy; vaccine; metastasis; ds.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis are
                                                  Disclosure;
                                                                    useful for metastasis
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                                                3071pp +
                                                 Sequence Listing; English
                                                                             antigen polypeptides, cancers and
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diagnosis and

quantitating a polypeptide in tissue,

as

molecular

weight markers

and

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or

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Best Local
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                                                                                                                                                  New isolated polynucleotide and diagnostics, forensics, gene map responsible for genetic disorder biodiversity
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                                                                                                                        Claim
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P-PSDB; ABG07278.
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23-AUG-2000;
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifty.wipo.int/pub/published_pct_sequences.
Sequence 1185 BP; 344 A; 262 C; 295 G; 284 T; 0 other;
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Qy Query Match 0.8%; Score 22; DB 23; Length 1185; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 22; Conservative 0; Mismatches 0; Indels 1587 cacacgggggagaagccatttg 1608 0; Gaps 0;

Search completed: May 16, 2002, 10:45:05 Job time: 8490 sec

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TITLE
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                                                                                                              human.
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                                 tcagaggacacactcaggatagaaactttatgtgtatagggaatgtggtacagcctttag 2134
                                                                                                Ctttaatgataagtccaccctcatttcacaccagaggacacattcaggggaaaagccttt 1774
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                                                                                                                                                                 GCAAGGCTTTAGCCGGCAGTCACACCTCATTAGACACCAGAGGACACATTCAGGAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab.host="hH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
Technologies."
249 c 268 g 255 t 4 others
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/clone="IMAGE:5579278"
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601594255F1 NIH_MGC_9 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCN811 row: m column: 13
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Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
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BE741389
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                                                                                                                                                                                                                                                287
                                                                                                                                                                                                                                        /tissue_type="adenocarcinoma cell line"
/lab_host="DH108 (phage-resistant)"
/lab_host="DH108 (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
87 a 233 c 293 g 257 t 1 others
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/clone_lib="NIH_MGC_9"
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/db_xref="taxon:9606"
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Eutheria; Primates;
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99.8%;
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                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
PHRAP suite: Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu
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                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_ESTs: 2823003.3prime
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 590)

NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
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AW245709
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2823003.5prime NIH_MGC_7
                                            Plate:
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           quality sequence stop:
Location/Qualifiers
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/note="Organ: lung; Vector: pOTB3; Site_1: XhoI; Site_2: Forexi; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 127 c 161 g 110 t
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/cell_line="MGC3"
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/clone_lib="NIH_MGC_7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/clone="IMAGE:5493685"
/clone=1b="NIH_MGC_67"
/closue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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gataggggtgggtacctggtgaaaccccaaccttaaagctgaagacagtcccggctaaatc
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National Cancer Institute, Cancer Genome Ana
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2312801"
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/lab_host="DH10B"
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Unpublished (1999)
Contact: Wambutt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKFZp586I0320_r1 586 (synonym: DKFZp586I0320, mRNA sequence. AL047439
                                                                                                                                                                                  Berlin-Charlottenburg, GERMAN Location/Qualifiers
                                                                                                                                                                                                          This clone (DKFZp586I0320) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg
                                                                                                                                                                                                                                             sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                   /clone="DKFZp586I0320"
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/dev_stage="adult"
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                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg,
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/db_xref="taxon:9606"
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                      /organism="Homo sapiens"
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cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                     1 (bases 1 to 558)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae
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BE220142.1
Eukaryota; Metazoa;
Mammalia; Eutheria;
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hv67f07.x1 NCI_CGAP_Lu24
                                     Homo sapiens
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//note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
                                                                                            GI:8907460
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99.8%;
 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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7.7e-248;
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CTGCAGTGAGGAGAGAAATCACCCTGCTGTGGGGGGTTGGGGGACCACTCCCTGCATCCCCT
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be come distribution the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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Seq primer: -40UP from Gibco
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/lab_host="https:"/lab_host="https:"/lab_host="https:"/lab_host="https://lab_host="https://lab_host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.host="https://lab.
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/clone_lib="NCI_CGAP_Lu24"
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Pred. No. 1.4e-242;
0; Mismatches 1;
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                                                                                                                                    734 acagtccaaggaagacaacacagtggtggatatagggtccagccctgaacggagggcaga 793
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                                      TCTAGAGGAAACAGACAAAGTATTGCATGGTTTAGAAGTCTCAGGATTTGGAGAAATCAA
                                                                                                                  ACAGTCCAAGGAAGACAACAGTGGTGGATATAGGGTCCAGCCCTGAACGGAGGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-HT0606-030
400-001-cl0&t3=2000-04-03&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Ge
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+55-11-2707001
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                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                         /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="HT0606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Eutheria;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                 primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 447.
               libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Scores NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1:
                                                                                                                                                /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
                                                                                                                                                                                                                       /clone="IMAGE:3523123"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                             /lab_host="DH10B"
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147720-148103,
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RESULT 12
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Butheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 505)

1 (bases 1 to 505)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Property Control of the control of
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hw24d02.x1 NCI_CGAP_Kid11 Homo:
                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                           Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
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Library Preparation: M. Bento
Library Arrayed by: Greg Lennc
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Pred. No. 6.6e-230;
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DEFINITION

UI-HF-BKO-aaf-c-03-0-UI.rl NIH\_MGC\_36 IMAGE:3053549 5', mRNA sequence.

Homo

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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can b found through the I.M.A.G.E. Consortium/LLNL, send email to:
AW401692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3183843"
/clone_lib="NCI_CGAP_Kid11"
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/db_xref="taxon:9606"
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TITLE
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AW401692.1
EST.
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution informa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 486)
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primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon;9606"
/clone="IMAGE:305349"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
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/cell_line="MGC85"
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Pred. No. 3.6e-225;
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Best Local
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                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%;
nes 419; Conservative
                                                                                                                                                                                                                                                                                     atcctcatactgaattgagaacctgtcttcccatttggtgttgctttcctccgattgatcc
                                                                                                                                                                                     gcagataggggtgggtacctggtgaaacccaaccttaaagctgaagacagtcccggctaa 2448
                                                        CAACCCTTCACCTATTTTACGTATACCTGCCCTTTCCTAATTGGTTTTTTACACTGCTGTG
                                                                     caacccttcacctattttacgtatacctgccctttcctaattggtttttacactgctgtg
                                                                                                                ATCCTCATACTGAATTGAGAACCTGTCTTCCCATTTGGTGTGCTTTCCTCCGATTGATCC
                                                                                                                                                                       GCAGATAGGGGTGGGTACCTGGTGAAACCCAACCTTAAAGCTGAAGACAGTCCCGGCTAA
                                                                                                                                                                                                                                TGGTGGGTTGTGGAAACCCCGGTCAGGTAATGATAGTGGCAGGAGGCAGTCAAATGCCCCAG
                                                                                                                                                                                                                                           tggtgggttgtgggaaacccggtcaggtaatgatagtggcaggaggcagtcaaattgcccag 2388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens cDNA HTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome
351 Guo Shoujing Road, Zhangji
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCAGAAGTCACACCTCATCAGACACTT
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AV720986.1
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Li,N., Qian,B., Liu,F., Qu,J., Gao,
.S., Gu,W., Tu,Y., Jia,J., Fu,G., R
Chen,J., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="HTBBIC05"
/clone_lib="HTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .486
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Pred. No.
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,X., Cheng,Z., Xu,
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Xu,Z., Zeng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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Best Local :
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                                                                                                                                                                                                                                                                gaattgctggctcattttcaggagccctgcccttcctcactgtggatggtgggttgtgga
                                                             ttttacgtatacctgccctttcctaattggtttttacactgctgtgcccaccttttgagt
                                                                                                                                                                                                                                                    GAATTGCTGGCTCATTTTCAGGAGCCCTGCCCTTCCTCACTGTGGATGGTGGGTTGTGGA
                                                                                                                                                                                                                                                                                                    TTTTACGTATACCTGCCCTTTCCTAATTGGTTTTTACACTGCTGTGCCCACCTTTTGAGT
                                                                                                                                                                                                    AACCCGGTCAGGTAATGATAGTGGCAGGAGGCAGTCAAATGCCCAGGCAGATAGGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis using a Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 613)
Hegde, P., Qi, R., Abernathy, K., Dharap, S.,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW964787 613 bp mRNA lir
EST376980 MAGE resequences, MAGH Homo sapiens
AW964787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of colon metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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207
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_nref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"
140 c 158 g 144 t
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1. .613
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Pred. No. 1.1e-206;
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Yeatman,T.J.
                                                                                                                                                                                                                                                                                                                                                                            Length 613;
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Best Local Similarity
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tcactttagctggaaatcaaacctcaaaacacaccagaggacacactcaggggttaaacc 1519
                                                                                                                                                                 aggagagaagccttacatttgcagggagtgtgagcaaggctttagccagaagtcacacct 1399
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                                                                                           AGGAGAGAAGCCTTACATTTGCAGGGAGTGTGAGCAAGGCTTTAGCCAGAAGTCACACCT
                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM274 row: i column: 02 High quality sequence stop: 635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 697)
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601286705F1 NIH_MGC_44 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   adaptor: GGCACGAG(G). Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologian 171 c 201 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Clone="IMAGE:3613513"
/Clone=lib="NIH_MGC_44"
/Clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; S:
EcoRI; cDNA made by oligo-dT priming. Directionally
EcoRI; cDNA made by oligo-dT priming. Directionally
Cloned into EcoRI/XhoI sites using the following 5'
Cloned into EcoRI/XhoI sites using the following 5'
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                                                                                                                                                                                                                                                                                                                14.9%;
                                                                                                                                                                                                                                                                                           Score 413; DB 10; I
Pred. No. 3.8e-206;
Prematches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and initial characterization of 5000 sequenced tags (ESTs) each from adult human normal osteoarthritic cartilage cDNA libraries osteoarthritis Cartilage 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                        Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
                                                                                                                                                                                                                                                                                                     UW2109
GlaxoSmithKline
                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 673)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG928720
HNC72-1-B2.R
                                                                                                                                                                                                                                                                       709 Swedeland Road, P.O. Tel: 610-270-7245 Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                         Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                           Similarity
                                                                                                                                                                                                                                                    primer:
                                                                                                                                               181
                                                                                   Conservative
                                                                                                                                                         /note="Vector: pSPORT I; Site_1:
Directional"
                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HMC (Human Normal Cartilage)
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
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AW513018/c
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                                                                                        quality sequence stop: 'Location/Qualifiers
                  /clone="IMAGE:2792381"
/clone_lib="WCI_CGAP_Ut1"
/tissue_type="well-differentiated
/tissue_type="well-differentiated
adenocarcinoma, 7 pooled tumors"
                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
          /lab_host="DH10B"
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Homo
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PCMV-SPORT6;
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.I.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sec
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/TLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AI276016
AI276016.1 GI:
            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq.primer: -40UP from Gibco
                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 481)
                                                                                                                                                                                                                                                                                                                                                                     qw08h02.x1 NCI_CGAP_Ut3
                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                Homo sapiens
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quality sequence
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99.8%;
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Pred. No. 2.
stop: 414
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Homo
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RESULT 2
AA450184
LOCUS
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SOURCE
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Best Local
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                                                                                            AUTHORS
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Mammaila, Lucand Mammaila, Lucand Lobases 1 to 451)

1 (bases 1 to 451)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Josephalier, L., Allen, M., Lennon, G., Marra, M., Martin, J., Kucaba, T., Lacy, M., Leptoe, M., Tan, F., Theising, B., White, Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                 AA450184

451 bp mRNA linear EST 04-JUN-199

ZX42e09.rl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
ZMAGE:/89160 5' similar to TR:G487783 G487783 ZINC FINGER PROTEIN
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                  EST
                                                                                                                                                                                                                   AA450184
AA450184.1 GI:2163934
                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone="IMAGE:1990515"
/Clone_lib="NCI_CGAP_Ut3"
/Clone_type="poorly-differentiated
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal. Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Average insert size 1.45 kb. Life Technologies catalog 11541-018" 127 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 8.7e-199;
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                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                 ATATTTGCAGAAAGTGTGGACGGGGCTTTAGTCGGAAGTCCAACCTTATCAGACATCAGA 63
                                                                                                                                                                                                                     TGTATCTCCATCCACCTGAAGGAGAATTGCTGGCTCATTTTCAGGAGCCCTGCCCTTCCT
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                                                                                                           AATGCCCAGGCAGATAGGGGTGGGTACCTGGTGAA
                                                                                                                                                                CACTGTGGATGGTGGGTTGTGGAAACCCGGTCAGGTAATGATAGTGGCAGGAGGCAGTCA
                                                                                                                                                                                                                                                                                        tagataccaaagtggagacattctgtgtgtgattatgcatgagactgtactggtaagact
                                                                                                                                                                                                                                                                                                                                AGTCATACTTCATCAGACACCAGAGGACACACAGAGTGCTGTGGCTTTTTCAGCCATTGC 183
                         AIO81665
ou63e06.sl NCI_CGAP_Br2
mRNA sequence
AI081665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) for seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
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Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Double-Stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 97 c 121 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson RK
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/db_xref="GDB:5986777"
/db_xref="taxon:9606"
/clone="MMAGE:789160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_11b="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/1ab_host="DH10B"
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Pred. No.
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Homo
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                         bp mRNA linear EST 27-AU sapiens cDNA clone IMAGE:1632514
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AUTHORS
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Insert Length: 862 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI_CGAP_BT1.1 Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/Clone_lib="NCI_CGAP_Br2"
/sex="female, pooled"
/tissue_type="breast"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Up from Glbco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
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Krizman,D., Kucaba,T., Lacy,M., ]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Thei
White,Y., Wylie,T., Waterston,R. and Wilson,R.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Barstead colon HPLRB7"
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hw31a02.x1 NCI_CGAP_Kid11 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
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National Cancer Institute, Cancer Genome Anat
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Seq primer: -40UP from Gibco.
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                                 /note="organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391), 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
              Fatima Bonaldo.
198 c 125
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/db_xref="taxon:9606"
/clone="IMAGE:3184490"
/clone_lib="NCI_CGAP_Kid11"
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
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BE746403
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CDNA Library Arrayed by: The I.M.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="NIH_MGC_9"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1:
EcoRI; cDNA made by oligo-dT priming. Direc
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                                                          cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 424)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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http://www.ncbi.nlm.nih.gov/ncicgap.
http://www.ncbi.nlm.nih.gov/ncicgap.
cancer Genome Anatomy
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-40ml3 fwd. ET from v sequence stop: 392.
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1635657"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                 GI:4308857
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Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1031 Std Error: 0.00
wq23a03.x1 NCI_CGAP_Kid11 Homo
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/db_xref="taxon:9606"
/clone="IMAGE:2134523"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicell"
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                                                                                                                                                 GTATTCCCCTATTCTGAGCCCATAAAAGACCCAGACTCAGCTGCAGTGAGGAGAAAATC
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Seq primer: -40UP from Gibco
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Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anat
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/clone="Image:2472076"
/clone="Image:2472076"
/clone=lib="NGI_GAP_Kidl1"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_GCAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cONAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Pred. No. 1.5e-184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail cDNA Library Preparation: M.B. Soares Lab Clone distribution: M.B. Cores Lab Clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW140124 501 bp mRNA linear EST 30-OCT-UI-H-BI1-aef-f-12-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719247 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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NCI_CGAP_Pr22, NCI_CGAP_CAP, NCI_CGAP_CO10,

NCI_CGAP_CO16, NCI_CGAP_Kid1, NCI_CGAP_LV12,

NCI_CGAP_EN12, NCI_CGAP_CO8, NCI_CGAP_LV24,

NCI_CGAP_BR12, NCI_CGAP_CO8, NCI_CGAP_LU24,

NCI_CGAP_BR12, NCI_CGAP_CO8, NCI_CGAP_LU24,

NCI_CGAP_BR12, NCI_CGAP_CO8, NCI_CGAP_LU24,

NCI_CGAP_LU19, NCI_CGAP_CO8, NCI_CGAP_LU26,

NCI_CGAP_CO10, NCI_CGAP_CO11

LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 12579611258631,

1145904-1522439); NCI_CGAP_CO10 Interpretation with a start of the s
6, /91-000.
TAG_LIB=NCI_CGAP_Kid5
                                                    was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The
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/db_xref="taxon:9606"
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                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail nih.gov
                                                                                                                                                                                                         Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 426)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                CDNA Library Preparation: Life Technologies, Inc
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                           AI650983
wa96d07.x1 NCI_CGAP_GC6
Bonaldo,
                           Tissue Procurement: Christopher A. R. Emmert-Buck, M.D., Ph.D.
                                                                     Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                  Tumor Gene Index
                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominic
1 (bases 1 to 486)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                  AI650983.1
                                                                                                                                                                                                                                                AI650983
                                                                                                                                                                                                                                                              mRNA sequence
                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                      Homo sapiens
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               cDNA Library Preparation:
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108 t
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/clone="IMAGE:2217535"
/clone_lib="NCI_CGAP_ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
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99.8%;
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Pred. No. 8.3e-180;
0; Mismatches 1;
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sapiens
               Bento
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ns cDNA
               Soares,
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                                                                                                                                                            Hominidae;
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clone IMAGE:2304013 3',
             Ph.D.,
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les 405; Conservative
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                                                                      naa29c11.x1 NCI_CGAP_Kid11 Homo
3', mRNA sequence.
BF476173
BF476173.1 GI:11546989
EST.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                     Homo sapiens
                                                       human
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2304013"
/clone_lib="NCI_CGAP_GC6"
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/lab_host="DH10B"
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 Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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Pred. No. 1.4e-175;
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                                                                                                                                                             mRNA
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   Hominidae;
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                                                                                                                                              IMAGE: 3257852
                  Euteleostomi;
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                   gttcttttgctcaataaaattcttttctaccca
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GTTCTTTGCTCAATAAAATTCTTTTCTACCCA
                                                                        GAAATCACCCTGCTGTGGGGGTTGGGGGACCACTCCCTGCATCCCCTCTCCACTGAGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Location/Qualifiers
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/clone="IMAGE:3257852"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10B"
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Pred. No. 1.8e-173;
0; Mismatches 2;
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                       tcactggaaattccatcttctaaaccaaaactcattgctcagctggagcgaggggaagcg
caacttagtccctcctgccctctgattttctccagtcagcaagctctcagccaacatgtg
                                                                               TCACTGGAAATTCCATCTTCTAAACCAAAACTCATTGCTCAGCTGGAGCGAGGGGAAGCG
                                                                                                                                  AGCCCTGCTCAGAGGACCCTGCACAGGGAGGTGATGCTGGAGACTTATAACCATCTGGTC
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Unpublished (1997)
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Zq96g04.rl Stratagene NT2 neuronal cDNA clone IMAGE:649878 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bmail: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@hmage.llnl.gov) for further i
Insert Length: 2813 Std Error: 0.00
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Mammalia; Eutheria;
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/clone="IMAGE:649878"
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/db_xref="GDB:5276467"
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Primates;
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               gaacctgtcttcccatttggtgtgctttcctccgattgatcccaacccttcacctatttt 2526
                                                                                                                                                    GAACCTGTCTTCCCATTTGGTGTGCTTTCCTCCGATTGATCCCAACCCTTCACCTATTTT
                                                                                ctggtgaaacccaaccttaaagctgaagacagtcccggctaaatcctcatactgaattga 2466
                                                                                                                                  CTGGTGAAAACCCAACCTTAAAGCTGAAGACAGTCCCGGCTAAATCCTCATACTGAATTGA
                                                                                                                                                                                                                                                                  400;
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1 (Cases 1 to 500)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies."
105 c 132 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2562929"
/clone_lib="NCI_CGAP_Mell5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="malignant melanoma, metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.2e-173;
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                             CAGGGAATGTGGGCGTGGCTTTCGCCAGCATTCACACCTGGTCAGACACAAGAGGACACA
                                                                                        CCTGAAGTCAAACCTCATTACCCACCAGAGGGCGCACACTGGGGGAGAAGCCTTATGTTTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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High quality sequence stop: 545.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incytte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcorI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 129 c 153 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3631603"
/clone_lib="NIH_MGC_44"
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Pred. No. 2.7e-170;
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www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiers
                                                                                         /clone="IMAGE:2424983"
/clone_lib="NCI_CGAP_Ufl"
/tissue_type="well-differentiated
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
                                                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT
                                   Average insert size 1.75 kb. Life Technologies catalog
                   11538-014"
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/db_xref="taxon:9606"
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qw32e05.xl NCI_CGAP_Ut4
                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                              AI289399
AI289399.1
                                    CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                  mRNA sequence.
         Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Hor
E 1 (bases 1 to 392)
E 1 (bases 1 to 392)
S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., The
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
L Unpublished (1997)
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AA218659.1
EST.
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                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                        Contact: Wilson RK
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/Clone="IMAGE:1992800"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma,
pooled tumors"
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Le,N., Lennon,G., Marra,M., Martin
Steptoe,M., Tan,F., Theising,B.,
.. and Wilson,R.
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AI361705
AI361705.1 GI:4113326
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1 (bases 1 to 395)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                              Homo sapiens
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/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (Kanamycin resistant)"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
_coRI; Site_2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/c1.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/db_xref="GDB:5276467"
/db_xref="taxon:9606"
/clone="IMAGE:649878"
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Pred. No. 1.1e-167;
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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   AW958936
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Location/Qualifiers
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M.D., Louis M. Staudt, M.D., Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2021887"
/clone_lib="NCI_CGAP_CIL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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B1256434
602974454F1 NIH_MGC_12 H
mRNA sequence.
B1256434
B1256434.1 G1:14810838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000) contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_maib="MAGE resequences, |
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
142 c 102 g 139 t
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  GI:14810838
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Pred. No. 4.5e-166;
0; Mismatches 1;
                                            Homo
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                                                         mRNA
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                                          clone IMAGE:5113861
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                                          EST 17-JUL-2001
E:5113861 5',
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                                                  tggattcaagaggga-gaagactccagactcctgtttgggagagtaagcaaaaatggcac 691
                                                                                                                                                                              | cactatccagaagatcagaaacaacagcaggatccattctgctttagtggcaaagcagaa
                                                                                                                                                                                                                                      agtcatctctctcagctgttttcaagtttatgggcaggaaatcctctccacctgggaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  453;
CACAGTGGTGGATATAGGGTCCAGCCCTGAACGG
                                                                                                           TGGATTCAAGAGGGACGAAGACTCCAGACTCCTGTTTGGGAGAGTAAGCAAAAAATGGCAC
                                                                                                                                                                 CACTATCCAGAAGATCAGAAACAACAGCAGGATCCATTCTGCTTTAGTGGCAAAGCAGAA
                                                                                                                                                                                                                         AGTCATCTCTCAGCTGTTTTCAAGTTTATGGGCAGGAAATCCTCTCCACCTGGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov http://image.lnl.gov plate: LLAM11276 row: k column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Site_2: Sall; Cloned unidirectionally. Primer: Oli Average insert size 1.4 kb. Library prepared by Lif Technologies."

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/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cervical carcinoma cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.3e-164;
0; Mismatches 0;
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                               tgtgcccaccttttgagtggtgcctttgcatacttacaaatcagtcaacgtgtattcccc 2624
                                                                                                                                                                           tattctgagcccataaaagacccagactcagctgcagtgaggagagaaatcaccctgctg 2684
                                                                                               atcccaacccttcacctattttacgtatacctgccctttcctaattggtttttacactgc
                                                                                                                                                                                                                             CCAGGCAGATAGGGGTGGGTACCTGGTGAAACCCCAACCTTAAAGCTGAAGACAGTCCCGG
                                                                                                                                                              CTAAATCCTCATACTGAATTGAGAACCTGTCTTCCCATTTGGTGTGCTTTCCTCCGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997.
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zx42e09.sl Soares_total_fetus_
IMAGE:789160 3', mRNA sequence
AA450119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq_primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997
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/clone="IMAGE:789160"
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/dev_stage="8-9 weeks"
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/db_xref="GDB:5986777"
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99.7%;
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Pred. No. 1.8e-163;
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TITLE
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                                                                   gaattgagaacctgtcttcccatttggtgtgctttcctccgattgatcccaacccttcac 2519
                 ctattttacgtatacctgccctttcctaattggtttttacactgctgtgcccaccttttg
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cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 457 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 378)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                             56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:910715"
/clone_lib="NCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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365; Conser
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AI159962
AI159962.1 GI:3693342
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IMAGE:1706443 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ggapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 655 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 364.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                              Conservative
                                                                                                                                                         same fetus as the fetal lung library,
NbHL19W."
1 70 c 105 g 85 t
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1706443"
                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                         /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                          /sex="unknown
                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_fetal_heart_NbHH19W"
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
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1. (bases_1 to 818)
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                             199
                   pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 980 Medical Center Drive Rockvill, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliangelifetech.com URL: http://fulllength.invitrogen.com" the contact of the
                                                                                                                                                                                                                                 cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I Eco RV sites of the convergence of the same convergence.
                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CSODF025Y022"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
                                                                                                                                                                                                                                                                                                                                         /note="Organ: Fetal brain; Vector: pCMVSPORT 6;
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/db_xref="taxon:9606"
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sapiens cDNA clone CS0DF025Y022 3
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                                                                                                                     Center Drive Rockville 610 8371 Email :
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Query Match Best Local Similarity

11.4%; 99.2%;

Score Pred.

315;

5; DB 9; 2e-154;

Length 818;

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AUTHORS
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Contact: Wilson RK
Washington University Schoc
4444 Forest Park Parkway, E
Tel: 314 286 1800
Fax: 314 286 1810
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                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.
Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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                                                             sequence.
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                              Homo sapiens
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 Eukaryota;
Mammalia;
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/db_xref="GDB:565059"
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Insert Size: 769
High quality sequence stops: 23
Source: IMAGE Consortium, LLNL
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Washington University Sche
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 769 Std Error: 0.00
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Hillier, L., Clark, N.,
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Location/Qualifiers
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//lab_hos
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/sex="Female"
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/db_xref="GDB:3818529"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 311; DB 10;
Pred. No. 2.3e-152;
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Best Local Similarity
Matches 408; Conserv
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tcagctgcagtgaggagagaaatcaccctgctgtggaggttgggggaccactccctgcatc
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies
, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
Consortium DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: polyT not
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 410) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Site_2: NotI; Cloned unidirectionally. Primer:
Library constructed by Life Technologies."
a 86 c 111 g 96 t 1 others
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co17"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW139497 383 bp mRNA UI-H-BII-ade-e-08-0-UI.sl NCI_CGAP_Sub3
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 52-178, >MER52#Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
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          //Ilab_host="MCI_CGAP_SUB3"
//lab_host="MCI_CGAP_SUB3"
//lab_host="McI_CGAP
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/clone_lib="NCI_CGAP_Sub3"
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  /db_xref-"taxon:9606"
                       /organism="Homo sapiens"
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2409 ggtgaaacccaaccttaaagctgaagacagtcccggctaaatcctcatactgaattgaga
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                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-HT0256-
080100-012-08&t3=2000-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence start: 661.
                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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Fax: +55-11-2707001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TAG_TISSUE=germ cell
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a 69 c 107 g
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                                                                                                                 cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM784 row: f column: 05
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1041)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE798936 1041 bp mrNA linear EST 20-5 601583719F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937924
                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/dev_stage="Adult"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CNNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Yamakido,M. and Watanabe,H.
The Kruppel-type Zinc Finge
Cancer by Exposure to Plati
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Direct Submission
Submitted (13-MAY-1998) Osamu Katoh, Res. Inst. Radiation Biology
and Medicine, Hiroshima Univ., Department of Environment and
Mutation; Kasumi 1-2-3, Minami-Ku., Hiroshima, Hiroshima 734-8553,
Japan (E-mail:katoho@mcai.med.hiroshima-u.ac.jp,
Tel:+81-82-257-5817, Pax:+81-82-256-7104)
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TYNHLYSLEIPSSKPKLIAQLERGEAFWREEERKCPLDLCPESKPEIQLSPSCPLIFSS
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/note="The HKR1 protein is similar to Kruppel-type zinc finger transcription factor and has Kruppel-associated t (KRAB): A and -B box at the N-terminus(nucleotides 193-390) followed by 13 C2H2-type zinc finger domain at the C-terminus(1020-2084)."
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Db	1320 1320	61 agaagcottatgtttgcagggaatgtgggcgtggctttcgccagcattcacacctggtca 	126 126	da Qy
- Db	1260 1260	01 gtgggcagagetttageetgaagtcaaaceteattaeeccaceagagggegeacaetgggg 	120 120	D 40
Db Ov	1200 1200	41 cgaacctctttacacatcagcggacacactcagggctcaagccttatgtgtgcaaggaat	114 114	Qy db
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Ov Db	1080 1080	21 tgtgcagggaatgtgggcgaggctttacgtggaagtcaaacctgatcacacatcagagga 	102	Db Qy
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                                                                                                                                                                                              Direct Submission
Submitted (24 OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
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1 Isogai, T., Otsuki, T. and Sugiyama, T.
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precursor cells treated 2-weeks mitotic
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Query Match
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2344; Conservative 0; Mismatches 2; Indels 0; Gaps cagaatcgaagccagaattcaacttagtccctccttgccctctgatttctccagtcagc 486		266	ttgggagagtaagcaaaaatggcacttcaaaggcactttccagcccacctgaagaac 	y 667 b 126701	Db dd	
2344; Conservative 0; Mismatches 2; Indels 0; Gaps cagaatcgaagccagaattcaacttagtccctcctgccctctgattttctccagtcagc 486		2670	cattctg          CATTCTG	y 607 b 126761	Db Dy	
2344; Conservative 0; Mismatches 2; Indels 0; Gaps cagaatcgaagcagaattcaacttagtccctcctgccctctgattttctccagtcagc 486		2676	cagg	y 547 b 126821	da Vy	
2344; Conservative 0; Mismatches 2; Indels 0; Gaps  cagaatcgaagccagaaattcaacttagtccctcctgcctctgattttctccagtcagc 486		82	aageteteageeaacatgtgtgggetgagteateteteteagetgtttteaagtttatgg 	1268	Qy db	
2344; Conservative 0; Mismatches 2; Indels 0; Gaps		88	aacttagtccctcctgccctctgattttctccagtc 	1269	Qy	
nal Cimilarity QQ QQ. Dro	••	ps	cal Similarity 99.9%; Pred. No. 0; 2344; Conservative 0; Mismatches 2; Indels 0; G	Best Lo		

2586	acgtatacctgccctttcctaattggtttttacactgctgtgcccaccttttgagtggtg	2527	Qy
124782		124841	Db
2526	gaacctgtcttcccatttggtgtgctttcctccgattgatcccaacccttcacctatttt	2467	Qy
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124902		124961	
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124962		125021	Db
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125022		125081	Db
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125202		125261	da
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125862	CAGAATGTGGGCGTCACTTTAGCTGGAAATCAAACCTCAAAACACACCAGAGGACACACT	125921	Db

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Consensus quality: 225569 bases at least Q30
Consensus quality: 235428 bases at least Q20
Consensus quality: 232428 bases at least Q20
Estimated insert size: 250510; agarose-fp estimation
Estimated insert size: 249417; sum-of-contigs estimation
Quality coverage: 9.03 in Q20 bases; agarose-fp estimation
Quality coverage: 9.07 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253217)
DOE Joint Genome Institute.
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Homo sapiens chromosome 19 clone CTD-3220F14, WORKING DRAFT
SEQUENCE, 39 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Summary Statistics
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AC016590.6 GI:13699590
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                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved
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/db_xref="taxon:9606"
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43409; gap of unknown length
48185: contig of 4776 bp in let
48285: gap of unknown length
55626: contig of 7341 bp in let
55726: gap of unknown length
65781: contig of 10055 bp in let
65781: contig of 3792 bp in let
65773: gap of unknown length
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agaggacacattcaggagagaagccttacatttgcagggagtgtgagcaaggctttagcc
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76550		76491	
2406	cggtcaggtaatgatagtggcaggaggcagtcaaatgcccaggcagataggggtgggt	2347	Qy
76490		76431	Db
2346	tgotggotcattttcaggagocotgcocttcctcactgtggatggttggggaaacc	2287	Qy
76430		76371	Db
2286	tgtgattatgcatgagactgtactggtaagacttgtatctccatcca	2227	Qy
76370		76311	Db
2226	cacacacagtgctgtggctttttcagccattgctagataccaaagtggagacattctgtg	2167	Qy
76310		76251	Db
2166	tgtatagggaatgtggtacagcctttagccaggagtcatacttcatcagacaccagagga	2107	. Qy
76250		76191	
2106	ttagtcggaagtccaaccttatcagacatcagaggacacactcaggatagaaactttatg	2047	Qy
76190		76131	Db
2046	gacaccagaggacacattcaggagagaaqccttatatttgcagaaagtgtggacgggggct	1987	Qy
76130		76071	Db
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1926	glgggcaaggcttttgtgctaagttaactctcattaaacaccagagagcacacgcagggg	1867	. Qy
76010		75951	
1866	agaagcctaacctgtttaggcacaagagggcacactcaggtgcctttgtgtgcagggagt	1807	Qy
75950		75891	Db
1806	agaggacacattcaggggaaaagccttttatgtgcagggagtgtggcagaaggtttcggc	1747	Qy
75890		75831	Db
1746	catttgtatgtgctgagtgtggacgaggctttaatgataagtccaccctcatttcacacc	1687	Qy
75830		75771	Db
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1626	ttaacaaacaccagaggtcacacacgggggagaagccatttgtatgta	1567	Qy
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75650		75591	Дъ
1506	cagaatgtgggcgtcactttagctggaaatcaaacctcaaaacacaccagagggacacact	1447	Qy
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Direct Submission
Submitted (12-MAR-2001) National Institutes of Health, Mammalian Submitted (MCC), Cancer Genomics Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer Tractitute. 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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Mol. Cell. Biol. 8, 3104-3113 (1988)
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Genome Center at Shanghai, 315 Guo
Shanghai 201203, P. R. China
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HTG; HTGS_PHASE1; HTGS_DRAFT
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        Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                     HOMO Sapiens chromosome 4 clone RP11-618K19, WORKING SEQUENCE, 3 unordered pieces.
                                                                 Submitted (01-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 12, 2002 this sequence version replaced gi:17921273.
                                                                                                                      Waterston, R.H.
Direct Submission
                                                                                                                                                                                     Waterston, R.H.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 161625)
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                           Unpublished
Web site:http://genome.wustl.edu/gsc/index.shtml
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/clone="RP11-420a23"
26050 c 26300 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length
89215: contig of 3160 bp in length
gap of unknown length
94479: contig of 5264 bp in length
103136: contig of 8657 bp in length
gap of unknown length
113254: contig of 10118 bp in length
gap of unknown length
130351: contig of 17097 bp in length.
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contig of 5588 k
gap of unknown ]
contig of 5890 k
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contig
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of 2024
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3 DRAFT
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                                                                                             Louis,
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Ding, H.,

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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
                       REFERENCE
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                                                                                                                                                                                                                                               RESULT 11
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Best Local Similarity 100.0%; Pred. No. 2.4e-09;
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Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 160310 bases at least Q40
Consensus quality: 160620 bases at least Q30
Consensus quality: 160738 bases at least Q20
Insert size: 164000; agarose-fp
Cuality coverage: 7.76 in Q20 bases; agarose-fp
Quality coverage: 8.11 in Q20 bases; sum-of-contigs
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164264)
                                                                                                                                                   Homo sapiens chromosome 3 clon SEQUENCE, 14 unordered pieces. ACO34197
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                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                AC034197.3 GI:8101273
                                                                                               human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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115854
115954
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115954. 161625
/note="assembly_name:Contig25"
a 31872 c 31765 g 50185 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig24
clone_end:SP6
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/db_xref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig26
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3123: gap of unknown length
115853: contig of 112730 bp in length
115953: gap of unknown length
161625: contig of 45672 bp in length.
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                                                                                                                                                                                                         164264 bp
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                                                                                                                                                                                    264 bp DNA linear clone RP11-72801 map 3p,
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WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Yang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                   12939
13039
19152
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24785
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32378
32378
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41546
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                                                                                                                                                                                                                                                                                  2044
2144
4408
4508
5591
5691
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Sequencing vector: pUC18: 100% of reads chemistry: Dye-terminator: ET 55% of reads chemistry: Dye-terminator: ET 55% of reads chemistry: Dye-terminator: Big Dye; 45% of reads chemistry: Dye-terminator Big Dye; 45% of reads chemistry: Dye-terminator Big Dye; 45% of reads chemistry: 15901 bases at least 040 consensus quality: 159151 bases at least 030 consensus quality: 165125 bases at least 020 consensus quality: 165125 bases at least 030 consensus quality: 165125 bas
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On May 29, 2000 this sequence version replaced gi:7644466
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Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,R., Wang,R., Wang,Y., Wang,J., Wang,Y., Wang,J., Wang,Y., Wang,R., Wang,X., Wang,Y., Wang,Y., Tao,R., Wang,Y., Wang,Y., Wang,Y., Zhang,Y., 
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* This record will be updated with the finished sequence
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Center code:Beijing
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http://www.genomics.org.cn
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2043: contig of 2043 bp in length
2143: gap of unknown length
4407: contig of 2264 bp in length
4507: gap of unknown length
5590: contig of 1083 bp in length
5690: gap of unknown length
8894: contig of 3204 bp in length
12938: contig of 3944 bp in length
12938: contig of 3944 bp in length
13038: gap of unknown length
13038: gap of unknown length
19151: contig of 6113 bp in length
14784: contig of 5533 bp in length
24784: gap of unknown length
32377: contig of 7493 bp in length
32477: gap of unknown length
41545: contig of 9068 bp in length
41645: gap of unknown length
41645: gap of unknown length
50978: gap of unknown length
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SOURCE
ORGANISM
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LOCUS
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 3 clone RP11-208K18 map 3p, SEQUENCE, 7 unordered pieces.

AC069265
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo: 1 (bases 1 to 165379)
Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,J., Li,J., Li,L., Li,L., Li,J., Li,J., Li,L., Li,J., Li,J.,
                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                      HTG;
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88889. .115986
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116087. .164264
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/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig17"
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100.0%; Pr
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b; Pred. No. 2.4
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                                                                           Ding, H.
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                                                                                                                                                                                                                                                                                         FEATURES
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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1975
8442
8542
20984
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21084
38291
38391
56761
56861
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Sequencing vector: pUC18; 100% of reads Chemistry: Dye-terminator: ET 55% of reads Chemistry: Dye-terminator Big Dye; 45% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 164602 bases at least Q30 Consensus quality: 165885 bases at least Q30 Consensus quality: 166968 bases at least Q30 Insert size: 162389; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang,L., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., N. Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center:Beijing Center
Center code:Beijing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromosome 3p genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Website:http://hgc.igtp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number be preserved.
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/note="assembly_name:Contig3"
1975. . 8441
/note="assembly_name:Contig4"
8542. . 20983
                                                                                                                                                                                                                   1. .1874
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                               /clone="RP11-208K18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1874: contig of 1874 bp in length
1974: gap of unknown length
20983: contig of 12442 bp in length
21083: gap of unknown length
38290: contig of 17207 bp in length
38390: gap of unknown length
56760: contig of 18370 bp in length
56860: gap of unknown length
93526: contig of 36666 bp in length
93626: gap of unknown length
165379: contig of 71753 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93526: contig of 36666
93626: gap of unknown 1
165379: contig of 71753
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[,X., Yu,J.
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Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                 Center:Beijing Center
Center code:Beijing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct
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Consensus quality: 146985 bases at least Q40 Consensus quality: 167923 bases at least Q30 Consensus quality: 182494 bases at least Q30 Insert size: 122192; sum-of-contigs Quality coverage: 3.83x in Q20 bases;sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 23, 2000 this sequence version replaced gi:7342324. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens chromosome 17 clone SEQUENCE, 13 unordered pieces.
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Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 141141 bases at least Q40
                                                                                                                                                                                                                                                                                    Center: Whitehead
Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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19001 27560: conti of 8500 bp in length

27561 27660: gap of 100 bp

27661 41935: contig of 14275 bp in length

41936 42035: gap of 100 bp

42036 58175: contig of 16140 bp in length

58176 58275: gap of 100 bp

58276 70930: contig of 12555 bp in length

70931 71030: gap of 100 bp

71031 87632: contig of 16002 bp in length

87633 87732: gap of 100 bp

87733 104759: contig of 17027 bp in length
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132 231: gap of 100 bp
232 4256: contig of 4025 bp in length
4257 4356: gap of 100 bp
6715: contig of 2359 bp in length
6716 6815: gap of 100 bp
6816 12854: contig of 6039 bp in length
12855 12954: gap of 100 bp
12855 12954: gap of 100 bp
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123864 123963: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7658384. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
Center project name: L5488
Center clone name: 308_J_14
Cen
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1 (bases 1 to 174405)
Birren, B., Linton, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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104860. .123863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2; 1; Pred. No. 9.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 148270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG 26-MAY-2000
WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                        misc_feature
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 177000; agarose-fp
Insert size: 173405; sum-of-contigs
Quality coverage: 4.8 in Q20 bases;
Quality coverage: 4.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144490 144589: gap of 100 bp
144590 174405: contig of 29816
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98516 121876; contig of 23361 bp in length
121877 121976; gap of 100 bp
121977 144489; contig of 22513 bp in length
144490 144589; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 173032 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48368 48467: gap of 100 bp
48468 63919; contig of 15452 bp in length
63920 64019; gap of 100 bp
64020 78259; contig of 14240 bp in length
78260 78359; gap of 100 bp
78360 98415; contig of 20056 bp in length
78361 98515; gap of 100 bp
98416 98515; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12912 13011: gap of
13012 22057: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 6450: contig of 6450 bp in length
6451 6550: gap of 100 bp
6551 12911: contig of 6361 bp in length
                                                                                                                                                                                                                                                                                                                                48468.
                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
22158. 32841
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
13012. .22057
                                        /note="assembly_fragment"
144590. .174405
                                                                                                                                                                                                                                                                                          64020
                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment" 32942. .48367
                                                                                                                         98516
                                                                                                                                   vector_side:left"
                                                                                                                                                               clone_end:T7
                                                                                                                                                                                                                        vector_side:right"
                                                                                                                                                                                                                                                clone_end:SP6
                                                                                                                                                                                                                                                            /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
  /note="assembly_fragment"
38223 c 37328 g 50956
                                                                              /note="assembly_fragment"
121977. .144489
                                                                                                                                                                              /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-308J14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13011: gap of 100 bp
22057: contig of 9046 bp in length
22157: gap of 100 bp
32841: contig of 10684 bp in length
32941: gap of 100 bp
48367: contig of 15426 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .174405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63919: cc.
                                                                                                                         .121876
                                                                                                                                                                                                                                                                                            .78259
                                                                                                                                                                                                                                                                                                                                   .63919
                                                                                                                                                                                                            .98415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 6361 bp in length
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dq
  1003 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agarose-fp
sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
AP001531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 127497 ATTGAGAACCTGTCTTCCCATTTGGTGTGCTTTCCT 127532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2462 attgagaacctgtcttcccatttggtgtgctttcct 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) On Aug 9, 2000 this sequence version replaced g1:8117372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 179792)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanaba,H. and Sakaki,Y.
Homo sapiens 179,792 genomic DNA of 18p11.3
published Only in DataBase (2000) In press
2 (bases 1 to 179792)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanaba,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator ET-amersham; 100% of program: Phrap; version 0.990329 Consensus quality: 171445 bases at least Q40 Consensus quality: 173267 bases at least Q30 Consensus quality: 175231 bases at least Q20 Insert size: 177492; sum-of-contigs
                      80877
89826
100085
108702
117937
125805
                                                                                                                                                         45696
55741
70173
                                                                                                                                                                                                                                                                                                         order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP001531 179792 bp DNA linear HTG 08-AUG-20 HOMO sapiens chromosome 18 clone RP11-772F18 map 18p11.3, WORKING
                                                                                                                                                                                                                        24476
                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists 24 contigs. The true order of the pieces is not known and their
                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 9.04x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: HumDraft1
Center clone name: RP11-772F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-772F18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP001531.3 GI:9757457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                preserved
                                                                                                                                                                                                                                                                                       as soon as it is available and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- Genome Center
                                                                                                         45595 contig of
55640 contig of
70072 contig of
80776 contig of
89725 contig of
99984 contig of
                                                                   108601
117836
                                               25704
                                                                                                                                                                                                                                          contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
1 contig of
6 contig of
4 contig of
8 contig of
2 contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HumDraft18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; pred. No.
                                                                                                                                                                                                                   24375 bp in length of 21120 bp in len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                       10604 bp in length
8849 bp in length
10159 bp in length
                                                                                                                                                         21120 bp in
9945 bp in
14332 bp in
10604 bp in
                                                                   8517
9135
                                             7768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       рв 2;
9e-09;
                                                                                       ďα
    9999
                                                                                                                                                                                                                                                                                       accession number will be
                                                                   in length
in length
                                                                                                                                                                             length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 174405;
                                          length
    length
                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   of
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as be

preserved

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## 134849 | 142692; contig of 7744 bp in length
## 134849 | 134848; contig of 7744 bp in length
## 134849 | 142692; contig of 7744 bp in length
## 13483 | 142792; gap of 100 bp
## 13493 | 151024; contig of 802 bp;
## 134949 | 142692; contig of 904 bp in length
## 13495 | 153124 | 16292; contig of 906 bp;
## 134949 | 142692; contig of 906 bp;
## 134949 | 142692; contig of 7744 bp in length
## 134949 | 142692; contig of 704 bp;
## 134949 | 142692; contig of 704 bp;
## 134949 | 142692; contig of 704 bp;
## 134949 | 142692; contig of 8232 bp;
## 151024 : contig of 8232 bp;
## 151025 | 151124 : gap of 100 bp
## 151125 | 151244; gap of 100 bp
## 151125 | 151244; gap of 100 bp
## 151125 | 151243; gap of 100 bp
## 15125 | 151243; gap of 100 bp
## 152504 | 152604; gap of 100 bp
## 152604 | 152604; gap of 100 bp
## 15260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142793 151024 contig of 8232 bp in length
151125 157334 contig of 6210 bp in length
157435 162933 contig of 5559 bp in length
163094 167067 contig of 3974 bp in length
167168 169460 contig of 2293 bp in length
167168 171662 contig of 2102 bp in length
17173 173150 contig of 1388 bp in length
17173 175114 contig of 1388 bp in length
175215 176145 contig of 1191 bp in length
175215 176405 contig of 1191 bp in length
176506 177563 contig of 1010 bp in length
17673 contig of 1010 bp in length
178774 178673 contig of 1010 bp in length
178774 179792 contig of 1010 bp in length
188774 179792 contig of 1010 bp in length
188774 179792 contig of 1010 bp in length
188774 179792 contig of 1010 bp in length
1887774 179792 contig of 1010 bp in length
188774 179792 contig of 1010 bp in leng
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24376 24475: gap of 100 bp
24476 45595: contig of 21120 bp in length
45596 45695: gap of 100 bp
45696 55640: contig of 9945 bp in length
   /organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map-"18p11.3"
                                                                                                                                                                                   Location/Qualifiers
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175214: gap of 100 bg
176405: contig of 1191 bg
176505: gap of 100 bg
177563: contig of 1058 b
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1093: gap of 100 bp
167: Gontig of 3974 bp in 16
167: gap of 100 bp
169460: contig of 293 bp in 16
1560: gap of 100 bp
171662: contig of 2102 bp in 16
173150: contig of 1108 bp in 16
173150: gap of 1108 bp in 16
173150: gap of 1108 bp in 16
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Homo sapiens chromosome ,
AC025211
AC025211.8 GI:15528921
                                                                                                                                                 HTG.
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                          Homo sapiens
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178774. .179792
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37736 c 3936
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177664. .178673
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175215. .176405
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171763. .173150
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167168. .169460
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163094. .167067
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142793 . 151024
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108702. .117836
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/note="assembly_fragment"
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55741. .70072
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24476. .45595
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151125. .157334
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125805. .134848
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117937. .125704
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34949. .142692
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Chordata;
Primates;
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39365 g 50954 t
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5. 9e-09;
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RP11-220C2, complete
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sequence.
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FEATURES source

173150:

178674 178773:

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REFERENCE
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AUTHORS
TITLE
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2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 8, 2001 this sequence version replaced gi:15431159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L.,
                                                                         SP6 end overlaps AC002119 [WICGR L141] by 43891 bp. 150793 bp of the overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                        Center project name Center clone name:
                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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       Location/Qualifiers
1. .150794
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                                                                                                                We will submit
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/note="430 qual SNGL region"
complement(15895. 15865)

/note="430 qual SNGL region"
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                                                                                                                                                                                                                                                                                              complement(12463
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complement/10/"
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complement//2/^
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4. .1580)
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ORGANISM
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                                         1 (bases 1 to 166650)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-253N19
                             Unpublished
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                        ACO87493 linear Homo sapiens chromosome 17 clone RP11-253N19 map 17,
                                                                                                                     Homo sapiens
                                                                                                                                                    HTG;
                                                                                                                                                               AC087493.3 GI:14192963
                                                                                                                                                                                                                                                                                                                                                                       Similarity
             (bases
                                                                                                                                                 HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L1MB2"
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complement(21644. 21658)
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complement(22343. 22535)
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complement/21for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="<30 qual SNGL region" complement(23400...23422)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alusx"
complement/oner:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alusg"
complement/10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="L1ME1"
complement/10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(17671
               1 to 166650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="L1MB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="(TG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluJb"
Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                     1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="AluJo"
1. .23399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="L1ME1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family=
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'="AluJb"
35
                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                     Score 34;
Pred. No.
 Nusbaum, C.,
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .17984)
                                                                                                                                                                                                                                                                                                                                                                     DB 9; 1
1.3e-07
Lander, E., Allen, N., Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                   Length 150794;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                           HTG 24-MAY-2001
, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                 FEATURES
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                              misc_feature
                                                                                                                                   source
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Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riey, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalnoun, J., Zembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:13123255. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently 
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: Li1973

Center clone name: Li1973

Center clone name: 253_N_19

Center clone name: 253_N_19

Center clone name: 253_N_19

Sequencing vector: Plasmid; n/a; 100% of reads

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 165769 bases at least Q40

Consensus quality: 165122 bases at least Q30

Consensus quality: 166247 bases at least Q20

Insert size: 16350; sum-of-contigs

Quality coverage: 11.0 in Q20 bases; agarose-fp

Quality coverage: 10.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 11793: contig of 11793 bp in length
11794 11893: gap of 100 bp
11894 33667: contig of 21774 bp in length
33668 33767: gap of 100 bp
33768 97497: contig of 63730 bp in length
97498 97597: gap of 100 bp
97598 166650: contig of 69053 bp in length.
                                                 /clone_lib="RPCI-11 Human Male
1. .11793
                                                                                                                                                                            /map="17"
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
note="assembly_fragment"
                                                                                                                                            /clone="RP11-253N19"
                                                                                                                                                                                                                              /chromosome="17"
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SOURCE
ORGANISM
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AC008106
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AUTHORS
                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39715 TGAGAACCTGTCTTCCCATTTGGTGTGCTTTCCT 39682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2464 tgagaacctgtcttcccatttggtgtgctttcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Haeford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLauphlin, J., McMaris, N., McKernan, K., Mychalecky, J., Mellai, M., Morris, W., Morrow, J., Mychalecky, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, B., Roberts, D., Roy, A., Severy, Stange-Thomann, M., Stopa, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, J.
                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                         Submitted (22-JUL-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 4, 2000 this sequence version replaced gi:7329486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo. 1 (Dases 1 to 218922)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, 34 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 17, clone CTD-3008D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC008106.3 GI:9966323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 218922)
Center project name: L900
Center clone name: 3008_D_3
Center clone name: 3008_D_3
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-primer-amersham; 100% of reads
                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                        Center code: WIBR
                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center
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1 33076 c 32370 g
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97598. .166650
/note="assembly_fragment
clone_end:T7
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33768. .97497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11894.
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100.0%;
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                                                                                                                                                                                                                                   Genome Center
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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CTD-3008D3 map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                              for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roy, A., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagner, A.,
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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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* consists of 34 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
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102206 102305; gap of 100 bp 102306 11255; contig of 9250 bp if 111556 111655; gap of 100 bp 111656 120772; contig of 9117 bp if 120773 120872; gap of 100 bp 120873 129869; gap of 100 bp 129870 129969; gap of 100 bp 129970 143160; contig of 13191 bp if 129970 143160;
                                                                                                                                                                                                       54897 54996: gap of 100 bp
54997 61677: contig of 6681 bp
61678 61777: gap of 100 bp
61778 68042: contig of 6265 bp
68043 68142: gap of 100 bp
68143 76003: contig of 7861 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21135 21234: gap of 100 bp
21235 24428: contig of 3194 bp
24429 24528: gap of 100 bp
24529 27705: contig of 3177 bp
27706 27805: gap of 100 bp
27806 30106: contig of 2301 bp
                                                                                      92832 102205
102206 102305:
102306 111555
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12217 14183: contig of 1967 bp
14184 14283: gap of 100 bp
14284 17330: contig of 3047 bp
17331 17430: gap of 100 bp
17431 21134: contig of 3704 bp
21135 21234.
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92732 92831:
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Insert size: 215622; sum-of-contigs
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2690: c
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39635 39734: gap of 100 bp
39735 43767: contig of 4033 t
43768 43867: gap of 100 bp
43868 50104: contig of 6237 t
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12117
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2791 4012: cor
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13 6412: gap of 100 bp
13 8474: contin 100 bp
5 8574
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35466: contig of 5160 b
35466: gap of
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84035: gap of 100 bp
92731: contig of 8696 bp
92831: gap of 100 bp
92831: gap of 100 bp
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8474: contig of 2062 bp
8574: gap of 100 bp
10328: contig of 1754 bp
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54896: contig of 4692 k
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61778. .68042
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35467. .39634
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27806. .30106
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50205. .54896
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39735. .43767
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21235. .24428
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111656. .120772
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12217. .14183
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54997. .61677
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/db_xref="taxon:9606"
/chromosome="17"
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                                                                                                                                                                                                                                                                                                               Sequencing vector: M13: 798
Sequencing vector: M13: 798
Sequencing vector: plasmid; 218
Chemistry: Dye-primer ET; 798 of reads
Chemistry: Dye-terminator Big Dye; 218 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 16280 bases at least Q40
Consensus quality: 16280 bases at least Q30
Consensus quality: 162828 bases at least Q20
Insert size: 146000; agarose-fp
Quality coverage: 9.33 in Q20 bases; sum-of-contigs
Quality coverage: 8.80 in Q20 bases; sum-of-contigs
                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Aug 28, 2001 this sequence version replaced gi:15145259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0036B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston,R.H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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AC027607
AC027607.6 GI:15321552
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Homo sapiens chromosome 4 clone
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143261. .154541
/note="assembly_fragment"
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129970. .143160
1192: contig of 1192 bp in length
1292: gap of unknown length
72574: contig of 71282 bp in length
72674: gap of unknown length
162453: contig of 89779 bp in length
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Pred. No. 1.3e-07
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RP11-36B15, WORKING
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REFERENCE
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VERSION
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ORIGIN
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                                                                                                          COMMENT
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AC036185/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
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Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2362 agtggcaggaggcagtcaaatgcccaggcaga 2393
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                                                                                                                                                                                                                                                                  Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McLarim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roya, Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subzamanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Viel, R., M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vien, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wyman, D., Ye, W.J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wyma
                              On Jun 21, 2000 this sequence version replaced gi:7523854. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Granam,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Illev,I., Johnson,R., Jones,C., Kan,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boguslavkiy.L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Coliangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 171279)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171279 bp DNA linear HTG 21-JUN-
HOMO sapiens chromosome 4 clone RP11-679B6 map 4, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
ACO36185
                                                                                                                                            Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                      Young, G.,
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                    Submission
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33274 c 34864 g
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/db_xref="taxon:9606"
/chromosome="4"
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                                                                                                                                                                                                                                                      Zainoun, J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-36B15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .162453
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2e-06;
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                                  misc_feature
                                                                                                          misc_feature
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* 39.87 50077: contig of 100 bp

* 39.87 50077: contig of 10891 bp in length

* 50078 50177: gap of 100 bp

* 50178 61526: contig of 11349 bp in length
61527 61626: gap of 100 bp
61627 7529: contig of 13903 bp in length
75530 75629: gap of 100 bp
75630 91544: contig of 15915 bp in length
91545 91644: gap of 100 bp
91645 1008750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2936 4108: contig of 1173 bp in length
4109 4208: gap of 100 bp
4209 7507: contig of 3299 bp in length
7508 7607: gap of 100 bp
7608 13869: contig of 6262 bp in length
13870 13969: gap of 100 bp
13970 20810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 7.1 in Q20 bases; Quality coverage: 7.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 679_B_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 169879; sum-of-contigs
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136878 136977: gap of 100 b
136978 171279: contig of 34302
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108851 136877: cont
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1486 2835: contig of 1757
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                                                                             /note="assembly_fragment"
4209..7507
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1486. .2835
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/note="assembly_fragment"
7608. .13869
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                               RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Radarson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collymore, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iiev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schaner, S., Severy, P., Spancer, R., Rothman, D., Schaner, S., Severy, P., Spancer, R., Schaner, S., Severy, P.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                     Santos, R.,
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136978. .171279
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28994. 39086
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36049 c 36303 g 49499 t
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50178. .61526
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39187. .50077
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13970. .20810
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                     Schauer, S.,
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                     Severy, P.,
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2e-06;
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                     Spencer, B.
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Mammalia, Eucheria, Primates; Catarrhini; Homi
1 (bases 1 to 17313)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-1D6
                                                                                                                                                                                  AC016166.3 GI:10198377
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                            Homo sapiens clone RP11-1D6,
                                                                                                                                          Homo sapiens
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On Dec 6, 2001 this sequence version replaced gi:13959308
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Direct Submission
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                                                                                                                                                                                                                                AC016166
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52669 104066: contig of 51398 bp in length
104067 104166: gap of 100 bp
104167 140470: contig of 36304 bp in length
140471 140570: gap of 100 bp
140571 171601: contig of 31031 bp in length
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37206 c 38797 g 51317
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                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                            Primates; Catarrhini; Hominidae;
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                                                      (bases 1 to 173133)
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Insert size: 170133; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 156896 bases at least Q40 consensus quality: 165527 bases at least Q30 Consensus quality: 165527 bases at least Q30 Consensus quality: 168595 bases at least Q20 Tagent 5.0.10400.
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Center clone name: 1
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21793. 23722
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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148302: contig of 14409 bp in
18402: gap of 100 bp
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3435: contig of 3207 l
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                      Direct Submission
Submitted (25-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                               2 (bases 1 to 174701)
Waterston, R.H.
                                                                                          Unpublished
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                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174701)
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                        The sequence of Homo sapiens clone
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51267. .55890
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119061. .133793
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27451. .30128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:http://genome.wustl.edu/gsc/index.shtml
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52566. .73259
                                     /note="assembly_name:Contig12"
140254. .174701
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73360 .105109
/note="assembly_name:Contig11"
105210 .140153
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20567. .35544
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/db_xref="taxon:9606"
/chromosome="2"
/note="assembly_name:Contigl3"
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1. .174701
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73259: contig of 20894 bp in 1
73359: gap of unknown length
105109: contig of 31750 bp in 1
105209: gap of unknown length
140153: contig of 34944 bp in 1
140253: gap of unknown length
174701: contig of 34448 bp in 1
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20466: contig of 13557 bp in
20566: gap of unknown length
35544: contig of 14978 bp in
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Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 159440 bases at least Q40
Consensus quality: 165805 bases at least Q30
Consensus quality: 169022 bases at least Q30
Consensus quality: 169022 bases at least Q20
Insert size: 169000; agarose-fp
Insert size: 174679; sum-of-contigs
Quality coverage: 3.59 in Q20 bases; sum-of-contigs
Quality coverage: 3.59 in Q20 bases; sum-of-contigs
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On Aug 17, 2000 this sequence version replaced qi:9797840.
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Direct Submission
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Sequencing vector: plasmid; 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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be preserved
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                    10623:
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                                                                                                                                                                                                                                          vector_side:right"
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2719. .5227
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/db_xref="taxon:9606"
/chromosome="11"
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43030: contig of 5457 bp in ler
43130: gap of unknown length
49891: contig of 6761 bp in ler
49891: gap of unknown length
57329: contig of 7338 bp in ler
57429: gap of unknown length
66759: contig of 9330 bp in ler
66559: gap of unknown length
75716: contig of 8857 bp in ler
75816: gap of unknown length
84641: contig of 9025 bp in ler
75816: gap of unknown length
84641: contig of 10454 bp in ler
84641: contig of 10454 bp in ler
84641: contig of 10454 bp in ler
84641: contig of 18811 bp in ler
84641: contig of 1881 bp in ler
84641: contig of 1881 bp in ler
84641: contig of 18434 bp in ler
84641: contig of 18454 bp in ler
84641: contig of 18454 bp in ler
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84642: gap of unknown length
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
99063792
                                                                                                            Submitted (29-APR-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 on Aug 13, 199 this sequence version replaced gi:5001523:
                                                                                                                                                                                                                                 Direct Submission
Submitted (13-AUG-1999) Genome
University School of Medicine,
                                                                                                                                                                     Direct Submission
                                                                                                                                                                                     Waterston, R.
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Submitted (25-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Center project name: H_NH0150013
                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                Contact: sapiens@watson.wustl.edu
                                                Web site: http://genome.wustl.edu/gsc
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158057. .175833
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142500. .157956
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110407. .123845
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

The clone sequenced to the left is RP11-355F16. Actual start of this clone is at base position 1 of RP11-150013; actual end is base position 207362 of RP11-150013. NEIGHBORING SEQUENCE INFORMATION: at

FEATURES repeat\_region source /rpt\_family="L1" 438. .738 /rpt\_family-"Alu" 8876. .9591 /rpt\_family="Alu" 8227. .8472 /rpt 3775 /rpt\_ta 12040. /rpt\_family="Retroviral"
11784. .11949 /rpt\_: /rpt 3727 /rpt\_family="Alu" 739. .1003 /rpt /clone\_lib="RPCI-11" 13. .437 /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="2" 1. .207362 /rpt\_family="L2" 12095. .12288 /rpt\_family="L1" rpt\_family="(TA)n" /clone="RP11-150013" /map="2" ocation/Qualifiers \_family="(TTTA)n" \_family="L1" \_family="L1" \_family="L2" \_family="MER1\_type" \_family="Other" \_family="MIR" .12079 .10240.1145)

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26883
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25258
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33891
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19038. .19270
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15734
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13360. .13408
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38193. .38312
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17134. .18265
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12788. .13196
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VERSION
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nes 32; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 21, 2001 this sequence version replaced gi:12227321.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is annotated repeat sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: FMBI, Sw: SWISSPROT: Tr: TREMBI; Wp: WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from clone complete sequence. AL157944
                                                                                                                                                                                                                           Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1 RP5-1126B2 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2
                                                                                                            This sequence is the entire insert of clone RP5-1126B2 The true left end of clone RP1-600K12 is at 95393 in this sequence. The teleft end of clone RP11-170N11 is at 1258B1 in this sequence. The true right end of clone RP11-14M11 is at 52383 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human was generated from part be found to be continued by the Sanger Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
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39291. .39494
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39167. .39243
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38873_ .39166
                                                                                    Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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2e-06;
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sequencing vector: M13; 77%
Sequencing vector: plasmid; 23%
Chemistry: Dye-primer ET; 77% of reads
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167158 bases at least Q40
Consensus quality: 167434 bases at least Q30
                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H.
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168736 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 8 clone RP11-11A18, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Mar 15, 200
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/note="Sequence from overlapping clones dJ600K12(AL357142)
and bA170N11(AL354654) Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from overlapping clones dJ600K12(AL357142)
and bA170N11(AL354654) Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Single clone region. Assembly confirmed restriction digest data" 65516. .65548
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Assembly confirmed by restriction digest data"
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Single clone region. Assembly confirmed restriction digest data"
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Assembly confirmed by restriction digest"
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/clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                        1 to 168736)
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Pred. No.
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7.7e-06;
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AC024996/c
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Best Local
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(bases 1 to 177864)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H.,
Anderson,S., Baldwin,J., Barna,N., Bastlen,V., Beda,F.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                 Unpublished
                                                                               1 (bases 1 to 177864)
Birren,B., Linton,L., Nusbaum,C.
Homo sapiens chromosome 8, clone
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           Homo sapiens chromosome 8, AC024996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 154000; agarose-fp
Insert size: 168336; sum-of-contigs
Quality coverage: 8.04 in Q20 bases; agarose-fp
Quality coverage: 7.38 in Q20 bases; sum-of-contigs
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                           AC024996.6
                                                                                                                                                                                         human
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97372. .168736
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53297._.97271
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/note="assembly_name:Contig16
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29076 c 28902 g 55038 t
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/chromosome="8"
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14897:
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contig of 43975 bp in
gap of unknown length
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gap of unknown length
contig of 10571 bp in length
gap of unknown length
contig of 38199 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 2; Le
Pred. No. 7.6e-06;
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                                                                                                                                                                                                                                                                           177864 bp
                                                                                                                                                                                                                                                           64 bp DNA linear PRI 12-DEC-2 clone RP11-697C18, complete sequence.
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                                                                                    and Lander, E. RP11-697C18
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                                     Allen, N.,
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Biren, B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ginde,S., Gord,S., Goyette,M., Gardan,J., Gardna-Pierre,N., Ginde,S., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nordu,C., Norman,C.H., O'Connon,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Viel,R., Vo,A., Wilson,B., Wix, Wyman,D., Ye,W.J., Young,G., Direct Submission
                                                                                                                                                                       Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Norbu, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Constant, P., Gardyna, S., Constant, P., Constant, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johns
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                                                                                                                                       Direct Submission
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(12-DEC-2001) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
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Grant,G., Hagos,B., Heaford,A., Horton,L.,
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Stojanovic, N.,
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TITLE JOURNAL REFERENCE

AUTHORS

REFERENCE AUTHORS

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TITLE JOURNAL

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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997. .1033
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3277. .3318
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11089
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complement/671
            /rpt_family="LTR27"
complement/12cc"
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/rpt_family="MSTB-int"
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10879
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/rpt_family="L2"
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complement/8820
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11 Human Male BAC"
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                Martinstied, GERMANY

(Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp564F1422) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                                 Direct Submission Submitted (15-MAY-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2328)
Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                         AL049942.1
                                                                                                                                                                                                                                                                                                                                     Homo sapiens mRNA; cDNA AL049942
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             http://www.mips.biochem.mpg.de/proj/cDNA/.
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23207. .2
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24080
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complement(26347. .26643)
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complement(24332.
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21741. .21946
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/rpt_family="MER58C"
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complement(16656. .
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/rpt_family="L2"
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3. .17821
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Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jb, Tel:88-438-52-3951, Fax:81-438-52-3951, Pat:81-438-52-3951, Pat:81-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isoi Kawai Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H. Kawai Hio,Y., Saito,K., Nishikawa,T., Kikuchi,H., Kanda,K., Watsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
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oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell line:NT2 cDNA
clone_lib:NT2RP7 clone:NT2RP7004352.
                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                Oshima,A., Sugiyama,A., Kawakami,B.,
Nagahari,K., Masuho,Y., Nagai,K. and
                                                                                                                                                    Direct Submission
                                                                                                                                                                               2 (bases 1 to 2790)
Isogai, T., Otsuki, T. and Sugiyama, T.
                                                                                                                                                                                                                                                                                              NEDO human cDNA sequencing project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HOKTHSGEKPFNCKOCEKSTSLKABLLRHOWTHSGERPFNCKDCGRGFBKWGNLLTHO
HOKTHSGEKPFICISECOGFTWKSNLTHHWRIHSKEKPFVCQECKRGYTSKSDLTVHER
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RENDKSYNKHLKAHSGEKPFVCKECGRGYTNKSYVHYKRIEGEKPYWCDCBRGFSO
SNKSHLITHQRTHSGEKPFACRQKOSFSVKGSLLRHQRTHSGEKPFVCKDCBRGFSQ
KSTLVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEBKPFVCKDCGRGFIQKS
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X1-2blue; sites NotI + SalI"
/dev_stage="fetal"
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/protein_id="CAB43216.1
/db_xref="GI:4884186"
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/db_xref="taxon:9606"
/clone="DKFZp564F1422"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
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Pred. No.
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Isogai,T.
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Matches 29
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                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K., and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Economy, Trade and Industry of Dapan, Communication for Biotechnology (RAB); cDNA library Research Association for Biotechnology (RRI); cDNA library construction: Helix Research Institute (HRI) (supported by Japan construction: Helix Research Institute of Technology RAB, Key Technology Center, National Institute of Technology and HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                      Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligo capping; fis (full insert sequence). Homo sapiens teratocarcinoma cell_line:NT2 clone_lib:NT2RI2 clone:NT2RI2003220.
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29; Conser
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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                                                                            Evaluation; clone selection for full insert sequencing: RAB {\tt HRI} .
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA sequencing project
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                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="teratocarcinoma"
/clone_lib="NT2RP7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="NT2RP7004352"
/cell_line="NT2"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.gov Series: IRAL Plate: 39 Row: d Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nigri.nih.gov/
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Thongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Each Site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC021298 3273 bp mRNA li
Homo sapiens, zinc finger protein 337, clone
IMAGE: 4551314, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                          Zhang, L.-H. and Green, E.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                  identity to protein.
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/note="cloning vector: pmE18SFL3-mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction.-majorly NT2 neuron 714 c 831 g 718 t
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/cell_type="teratocarcinoma"
                                                      /db_xref="taxon:9606"
/clone="wcc.occo
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/clone="NT2RI2003220"
/tissue_type="Lung, large cell carcinoma"
/clone_lib="NIH_MGC_18"
                                                                                             /organism="Homo sapiens"
/db_xref="LocusID:26152"
                                                                                                                                                   Location/Qualifiers
1. .3273
                                                 /clone="MGC:29686 IMAGE:4551314"
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MGC:29686
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HS694B14/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS694B14 127867 bp DNA linear PRI Human DNA sequence from clone RP4-694B14 on chromosome 20p11.1-11.22 Contains a novel KRAB box protein with 18 zinc finger domains, a novel haloacid dehalogenase-like family protein similar to (archaea) bacterial proteins, putative novel genes, a novel pseudogene, ESTs, an STS, three CpG islands, complete sequence.
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127867)
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HTG; CpG island; haloacid dehalogenase; hydrolase; KRAB box;
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KQPFVCKECGRGFNWKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
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RHORTHSGEKPFVCKDCERSFSOKSTLVYHORTHSGEKPFVCRECGGGFIQKSTLVKH
QITHSGEKPFVCKDCGRGFIOKSTFLHORTHSEEKPYGCREGGRRFRDKSSVNKHLR
AHLGEKRFFCRDCGRGFTLKPNLTIHORTHSGEKPFMCKQCEKSFSLKANLLRHOWTH
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NPTEIDKULKGIENSRWGAFKOAERGQDFSKKMWIIHKKAHSKRKLFTGRECHQGFR
ENSALLLHQNTHTGEKSYVCSYCGRGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSK
SYLTVHERTHTGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYTNKSY
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/protein_ld="AAH21298.1"
/db_xref="Gi:18204656"
/translation="MGPQGARRQAFLAFGDVTVDFTQKEWRLLSPAQRALYREVTLEN
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Pred. No. 0.00013;
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2373. .2
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                                         complement(8265.
                                                                                                                                                                                                /note="Tandem repeat. region contains forced join and
single clone. HindIII digest suggests there is
approximately lkb missing from the tandem repeat."
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                                                                 /note="match:
                                                                                     complement(8211.
                                                                                                                                  complement(8206
                                                                                                                                                                                                                                                                      complement(7844. .8286)
                                                                                                                                                                                                                                                                                      /note="57 copies 2 mer ct 75% conserved"
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                                                                                                          /note="match: GSS:
                                                                                                                                                  /note="19 copies 2 mer ca 78% conserved"
                                                                                                                                                                                                                                                                                                                                     /note="44 copies 2 mer ct 73% conserved"
                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1B repeat: matches 6. .390 of consensus"
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/note="Alusx repeat: matches 1.
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/note="Alusc
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/clone="RP4-694B14"
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1. .127867
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                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 2634. .2743 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L1MC3 repeat: matches 7230. .7739 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 5924. .6022 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1. .306 of consensus"
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                       Em: AQ587567
                                                                                                          Em: AQ535283
                                                              Em: AQ507005"
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/note="match: 15114. .15332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13828. .14126
/note="AluJb repeat: matches 1.
complement(13929. .14330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13209. .13290
/note="MLTIF repeat: matches 243. .317 of consensus"
13319. .13366
/note="MLTIF repeat: matches 280. .327 of consensus"
13394. .13480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="FLAM_10737. .1107
                                                                                                                                                                 complement(15127.
                                                                                                                                                                                                                                                                                                                                                                                                                        complement(15066. .15246)
/note="match: GSS: Em:AQ807616"
complement(15089. .15356)
/note="match: GSS: Em:AQ490556"
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complement(15160..15332)
/note="match: STS: Em:G42
complement(15171..15346)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(15065. .15333)
/note="match: GSS: Em:AQ7
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/note="match: GSS: Em:AZ5
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13209. .13290
                                                         /note="match: 15156. .15348
                                                                                                                  /note="match: GSS:
complement(15135. .
                                                                                                                                                                                                                                /note="match: GSS: 15121. .15331
                                                                                                                                                                                                                                                                                                                                                 /note="match: 15109. .15332
                                                                                                                                                                                                                                                                                                                                                                               complement(15097
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15040. .15332
/note="Alusx repeat: matches 1.
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14937. .15009
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/evidence=not_experimental
                                                                                     /note="match:
15143. .15329
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15129. .15340
                                                                                                                                                                                                                                                                                                                                                                                             /note="match:
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14591. .14757
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15117. .15332
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                Em:G42878"
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15356)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Belveriy, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Cardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Meldrim, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-3B10
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                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                  Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2000 this sequence version replaced gi:7209490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Center project name: 3
                                                 Contact: sequence_submissions@genome.wi.mit
                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center
                                                                                                      Web site: http://www-seq.wi.mit.edu
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15216. .15353
/note="match: GSS: Em:AG014867"
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.15328)
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WORKING
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E, 15 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
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2703 4233: contig of 1530 bp in length
4233 4332: gap of 100 bp
4333 5881: contig of 1549 bp in length
5882 5981: gap of 100 bp
5882 5981: gap of 2073 bp in length
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/note="assembly_fragment
clone_end:T7
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11725. .15457
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1170. .2602
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/clone="RP11-3B10"
/clone_lib="RPCI-11 Human Male
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REFERENCE
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AC109473/c
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ORIGIN
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Best Local Similarity
Matches 29; Conserv
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                 Consensus quality: 174095 bases at least Q40 Consensus quality: 175269 bases at least Q20 Consensus quality: 175269 bases at least Q20 Estimated insert size: 174280; agarose-fp estimation Estimated insert size: 180970; sum-of-contigs estimation Quality coverage: 43.3 in Q20 bases; agarose-fp estimation Quality coverage: 41.7 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently 'consists of 9 contigs. The true order of the pieces 'is not known and their order in this sequence record is 'arbitrary. Gaps between the contigs are represented as 'runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                         Summary Statistics
                                                                                                                                                                                                                                                                                                           Center Project Name: 407551
Center clone name: RPCI-11_3B10
                                                                                                                                                                                                                                                                                                                                                          Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates;
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Homo sapiens chromosome 5 clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOE Joint Genome Institute.
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This record will be updated with the finished sequence
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124331. .170129
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31892 c 33160 g 50668
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100.0%; Pred. No. 0.00011;
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Db 177072 CCTGTCTTCCCATTTGGTGTGCTTTCCTC 177044
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Best Local
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Homo sapiens, clone MGC:20504
BC011862
BC011862.1 GI:15080170
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Brooks,S., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2823)
                                                                                               DNA Sequencing by: National Sequencing Center (NISC), Sequencing Center (NISC), Sequence (NISC), Maryland;
                                                                                                                              cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                          Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                       Web site:
                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                  Contact:
                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                         Contact:
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. 34865 c 35014 g 53844 t 811
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/db_xref="taxon:9606"
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9965: contig 0
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11302: contig 0
                                                                      nisc_mgc@nhgri.nih.gov
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BASE COUNT ORIGIN

Matches

FEATURES

REMARK COMMENT

SOURCE ACCESSION VERSION

ORGANISM

KEYWORDS

DEFINITION LOCUS BC011862 RESULT

REFERENCE

TITLE AUTHORS

JOURNAL

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Query Match
Best Local Similarity
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                                                                                                                                                                       Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M., Yamashita,H., Chiba,Y., Sujiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK055734 3055 bp mRNA linear Homo sapiens cDNA FLJ31172 fis, clone KIDNE2000051, similar to ZINC FINGER PROTEIN 133.
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Submitted (24-OCT-2001) Takao Iso
Genomics Laboratory; 1532-3 Yana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligo capping; fis (full Homo sapiens kidney cDNA
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                                                    Direct Submission
                                                                      2 (bases 1 to 3055)
Isogai,T., Otsuki,T. and Sugiyama,T.
                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                      Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguo
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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RTHSGEKHYVCRECRRGFSQKSNLIRHQRTHSNEKPYICRECGRGFCDKSTLIVHERT
HSGEKPYVCSECGRGFSRKSLLLVHQRTHSGEKHYVCRECGRGFSHKSNLIRHQRTH"
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ESNFITNPRTLLGKKPYICSDCGRSFKDRSTLIRHHRIHSMEKPYVCSECGRGFSQKS
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/product="Unknown (protein for MGC:20504)"
/protein_id="AAH11862.1"
/db_xref="GI:15080180"
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/clone_lib="NIH_MGC_46"
/lab_host="DH10B-R"
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/clone="MGC:20504 IMAGE:4328382"
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                                                                                                      Center: Joint Genome Institute
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Homo sapiens chromosome 5 clone SEQUENCE, 16 unordered pieces.
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NEDO human cDNA sequencing project supported by Ministry of Economy. Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end Role pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                  Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                            Direct Submission
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DOE Joint Genome Institute
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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Center Project Name: 531233
                        Project Information
                                                              Web site: http://www.jgi.doe.gov
                                                                                      Center Code: JGI
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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FPSPLQRQSASPRKGNMVVETEPSSAQRPNPVQLDKGLKELETLRFGAINCREYEPDH
NLESNFITNPRTLLGKKPYICSDCGRSFKDRSTLIRHHRIHSBEKPYVCSECGRGFSQ
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SEIRHQRTHSGEKPYVCLECGRSFCDKSTLRKHQRIHSGEKPYVCRECGRGFSQNSDL
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RTHSGEKPYVCSECGRGFSRKSLLLVHQRTHSGEKHYVCRECGRGFSHKSNLIRHQRT
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/tissue_type="kidney"
/clone_lib="KIDNE2"
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/db_xref="GI:16550537"
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/db_xref="taxon:9606"
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100.0%; Pr
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Pred. No.
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RP11-325C20, WORKING
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RESULT 40
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                                                                                   22636 ATTGATCCCAACCCTTCACCTATTTTAC 22663
                                                                                                2501 attgatcccaacccttcacctattttac 2528
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AF161800 62002 bp DNA linear HTG 13-JUN-2001 HOmo sapiens chromosome 8 clone XX-189m5 map 8q21.2, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 47683 bases at least Q40
Consensus quality: 55520 bases at least Q20
Consensus quality: 55520 bases at least Q20
Consensus quality: 56595 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 59952; sum-of-contigs estimation
Quality coverage: 5.17 in Q20 bases; agarose-fp estimation
Quality coverage: 13.8 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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5252
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/db_xref="taxon:9606"
/chromosome="5"
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/clone_lib="RPCI human BAC library
10746 c 10505 g 20606 t 1508
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100.0%; Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65236 bp ' DNA linear HTG 22-DE) Homo sapiens chromosome 17 clone CTD-2244F11 map 17, LOW-PASS SEQUENCE SAMPLING.
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUN-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany * NOTE: This is a 'working draft' sequence. It currently * consists of 1 conties. Gaps between the conties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schudy, A., Schilhabel, M., Schlegelberger, B., Drescher, B., Weber, J., Schattevoy, R., Menzel, U. and Rosenthal, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schilhabel, M.B., Baumgart, C., Blechschmidt, K., Dette, M., Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A. Siddiqui, R., Taudien, S., Wen, G., Korenberg, J., Rosenthal,
                                                                                                                          Unpublished
                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CTD-2244F11
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
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                                                                                                      (bases 1 to 65236)
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1 62002: contig of 62002 bp
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/db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * However, it should not be assumed that this clone
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8033: contig of 693 b
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75 17901: contig of 727 bp
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75 18706: contig of 715 bp
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17738: contig of 735 bp
17738: gap of 100
28427: contig
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9888: gap of 10
40623: contig of 7
7723: gap of 10
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21913: contig of 704 bp
12013: gap of 100 bp
22735: contig of 722 bp
22735: gap of 100 bp
2835: gap of 100 bp
3656: gap of 721 bp
3656: gap of 100 bp
24379: contig of 723 bp
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19523: contig of 707 bp
9623: gap of 100 bp
20307: contig of 684 bp
0407: gap of 100 bp
1109: contig of 702 bp
1209: gap of 100 bp
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41446: contig of
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157: gap of 100 bp
157: gap of 100 bp
38146: contig of 689 bp
                   346: gap
42259: c
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25134: contig of 655 bp in length
234: gap of 100 bp
25962: contig of 728 bp in length
062: gap of 100 bp
26803: contig of 741 bp in length
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66: contig of 720
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TITLE
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Submitted (04-MAY 2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1sA, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 8, 2001 this sequence version replaced gi:13751525.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)
                                                                                                                                                                                                                                                                                                                 sequence.
AL512489
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Mammalia; l
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28; Conserv
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5337: contig of 717 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases: Em; EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP11-44708 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr6 RP11-44708 is from the library R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tp://www.chori.org/bacpac/home.htm
TOR: pBACe3.6
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/note="FLAM_C repeat: matches 1.
9582. .10277
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/note="Charliela repeat: matches 1025. .1455 of consensus"
6632. .7214
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/note="17 copies 2 mer tg 85% conserved"
3664. 3969
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2590...262
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/note="AluSq repeat: matches 1.
complement(9091. .9549)
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/note="MER52A repeat: matches 1602. .1750 of 7543. .8513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="34 copies 2 mer at 75% conserved" 6233. .6631
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/db_xref="taxon:9606"
/chromosome="6"
                                                                         /note="MIR repeat: matches 118.
complement(12908. .13388)
                                                                                                              /note="20 copies 2 mer tt 87% conserved"
12790. .12897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="12 repeat: matches 2098. .2176 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="45 copies 2 mer ta 62% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
   /note="MIR repeat: matches 17.
13377. .14279
                                                                                                                                                                                                                                           note="match: GSS: Em:AQ728035"
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/note="LTR28 repeat: matches l. .608 of consensus"
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                                                                                                                                                                     note="match: GSS:
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                                                        'note="match:
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                                                      Em: AQ437578"
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                   .78 of consensus"
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                                                                                                                                                                                                        /note="MIR repeat: matches 13. .262 of consensus" 43855, .44065
                                                                                                                                                                                                                                                                                                                                                                                             /note="L1PA7
41074. .4161
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(35522 /note="match: GS 35729 . .41433
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note="liph1 repeat: matches -1537. .-412 of consensus"
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14124. .14355
                                                      /note="96 copies 2 45135. .45194
                                                                                             45003
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                                                                                                                                  44930
                                                                                                                                                                     /note="MLT1J repeat: matches 293.
44137. .44860
                                                                                                                                                                                                                                                          /note="L2 repeat: matches
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complement(35522. .36045)
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23505. .23963
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21514. .21663
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18033. .18161
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                                      /note="15 copies 4 mer
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                       .45237
                                                                                                                            LIPA/ repeat: matches
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20897
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                                                                                                        requests: clonerequest@sanger.ac.uk
On Jun 22, 1999 this sequence version replaced gi:4995635.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                              Submitted (22-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                     Blakey, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 3' end of a novel KRAB box protein gene, a novel C2H2 zinc finger domain protein gene, the SNRPB gene for small nuclear ribonucleoprotein polypeptides B and Bl (B') and the 3' end of the gene for a novel transglutaminase. Contains ESTs, STSs, GSSs and a
                                                                                            This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90220)
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47950. .47991
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47132. .47713
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/note="AluSg/x repeat: matches 113. .312 of consensus"
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60497. .60587
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Pred. No.
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20. Contains
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VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RP4-734P14 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP4-816K17 is at 1 in this sequence.
true left end of clone RP4-816K17 is at 90117 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; SWISSPROT: TT:, TREMBL; Wp:, WORMPEP; Information on the WORMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chr20
RP4-734P14 is from the library RPCI-4 constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Sw:Q02386 Sw:P51786 Sw:Q99676 Tr:C60792 Sw:Q0323 Tr:C92473 Tr:Q93KU4 Tr:C99974 Sw:C95201 Tr:C93LD3 Sw:C62396 Tr:C922X6 Tr:C15322 Tr:C9WVI0 Tr:C14913 Sw:C61751 Tr:C99P0L1 Tr:C99N42 Sw:C90UU3 Tr:P70591 Tr:C94886 Sw:C02975 Tr:C94892 Tr:C99ND1 Tr:C62977 Tr:C9Y2N8 Tr:C9Y2N9 Tr:C43296 Tr:C9NVW4 Tr:C9Y3N9 Tr:C9NR11 Sw:C60765 Tr:C95765 Tr:C99NW4 Tr:C9Y3N9 Tr:C9NR11 Sw:C60765 Tr:C95765 Tr:C9QYXT9 Tr:C9XSR1"
                                                                                                                                         /note="MER33 repeat: 4121. .4296
                                                                                                                                                                                                                                                                                                                                                                        /note="MER70B repeat: matches 267. .294 of consensus"
2150. .2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        match: ESTs: Em:BE791109 Em:AV740593"
/product="dJ734P14.1 (novel KRAB box protein)"
                                                                                  /note="AluSq repeat:
4822. .4952
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QETETTLANIVKSHLY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mmlpypSALGDQYWEEILLPKNGENVETMKKLTQNHKAKGLPSN
DTDCPQKKEGKAQIVVPVTFRDVTVIFTEAEWKRLSPEQRNLYKEVMLENYRNLLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5 are part of the same gene in the form determined isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(929. .1046,1247. .1305,1999.
/gene="dJ734P14.1"
                                                                                                                                                                                                                           /note="MER58B repeat: matches 2.
                                                                                                                                                                                                                                                                                   /note="AluSc repeat: matches
                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2288. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJb repeat: matches 5. .299 of consensus"
join(<780. .1046,1247. .1305,1999. .2125,2740. .28
/gene="dJ734P14.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP4-734P14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                       /note="FLAM_C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="dJ734P14.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="continued from dJ807J1.1 in Em:AL133339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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repeat:
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the same gene in the form of
                                                                                                                  matches 135.
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                                                                                                                                                                                                                                                                                      63.
     28.
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                                                          .133 of
                                                                                                                                                                                                                              .341 of consensus"
                                                                                                                                                                                                                                                                                      .303 of consensus"
                                                                                                                                                                       . 324
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                                                                                                               .310 of consensus'
     of.
                                                                                                                                                                       of
                                                          consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: ESTs: Em:AV686588 Em:AV686906 Em:AV688199 Em:AV684693 Em:AV698692 Em:AV691116 Em:AV691591 Em:AV684693 Em:AW2986692 Em:AV691116 Em:AV691591 Em:AV685942 Em:AW249885 Em:AIJ35243 Em:BE251006 Em:AV6859318 Em:AIJ090631 Em:AIJ022856 Em:BE057295 Em:AV659318 Em:BE255957 Em:AIJ022856 Em:BE057295 Em:AIJ141853 Em:BE255957 Em:AIJ023983 Em:AW152481 Em:AW0014719 Em:BE2579108 Em:BE375372 Em:AV720356 Em:T06312 Em:BE313012 Em:AW209561 Em:AW205046 Em:AW392867 Em:BE313012 Em:W90340 Em:AU399040 Em:W90339 Em:BE744885 Em:BE250978 Em:W90340 Em:AIJ19459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="protein homologies suggest that this gene and
.1 are part of the same gene in the form of a yet to
determined isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="dJ734P14.5"
<10150. .11663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2611.
<10150. .13007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7592. .7742
/note="L1MC4 repeat: matches 6190. .6343 of consensus"
7743. 7941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSp repeat: matches 1.
8331. .8396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1MC4 repeat: matches 6343. 8043. .8330
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7942. .8042
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6324. .6691
                                                                                                                                                                                     KPYVCSECGRGFSRKSLLLVHQRTHSGEKHYVCRECGRGFSHKSNLIRHQRTH"
complement(10354. .10858)
                                                                                                                                                                                                                               HQRTHSEEKPYLCRECGOSFRSKSILNRHQWTHSEEKPYVCSECGRGFSEKSSFIRHQ
RTHSCEKPYVCLECGRSFCDKSTLRKHGRIHSCEKPYVCRECGRGFSQNSDLIKHQRT
SLDEKPYVCRECGRGFEDKSTLIHERTHSGEKPYVCGECGRGFSRKSLLLVHQRTHS
GEKHYVCRECRRGFSQKSNLIRHQRTHSNEKPYICRECGRGFCDKSTLIVHERTHSGE
                                                                                                                                                                                                                                                                                                                           /translation="NFHSSAEPKPEIYTCSSCLLAFSCQOFLSQHVLQIFLGLCAENH
FHPCNSSPGHWKQGGQYSHSSACRPNPVQLDKGLKELEFLRFGÄINCREYEPDHNLESNF
RQSASPRKGNMVVETEPSAQRPNPVQLDKGLKELEFLRFGÄINCREYEPDHNLESNF
ITNPRTLLGKKPYICSDCGRSFKDRSTLIRHHRIHSMEKPYVCSECGRGFSQKSNLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein)"
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10150. .13007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/product="dJ734P14.5 (nove
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                                              /note="match:
12666. .13089
                                                                                            complement(12523
                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAC32827.1"
/db_xref="GI:13160045"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MC4 repeat: matches 6435. .6501 of consensus"
                                                                                                                  /note="LTR16A repeat: matches 216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .9650
                                                                                                                                                                GSS: Em:AQ594268"
                                                                      STS: Em: AA463461"
                          Em: AQ080563'
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AUTHORS
TITLE
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REFERENCE
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AF159227/c
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ORGANISM
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AF159227
                                                                                                                                     Submitted (05-FEB-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany On Feb 5, 2002 this sequence version replaced gl:16356843.
                                                                                                                                                                                                                                                                             Submitted (24-OCT-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany 4 (bases 1 to 109217)
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-JUN-1999) Genome Analysis; Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany 3 (bases 1 to 109217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wen,G., Baumgart,C., Blechschmidt,K., Dette,M., Jahn,N.,
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,
Siddiqui,R., Taudien,S., Schilhabel,M.B., Schlegelberger,B.
Siebert,R., Rosenthal,A. and Platzer,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF159227 109217 bp DNA linear Homo sapiens chromosome 8 clone GS1-225N9 map 8q24,
                                                                                                                                                                                                                                                                                                                                                   Wen,G. and Platzer,M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schudy, A., Blechschmidt, K., Weber, J., Schattevoy, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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1 (bases 1 to 109217)
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HTG; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                       Wen,G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                          Web site: http://genome.imb-jena.de/Contact: gscj-submit@genome.imb-jena.
  Center project name: H104
                                                                                              Center code: IMB
                                                                                                                  Center: Insitute of Molecular Biotechnoloy
                                                                                                                                                                                                                                                       and Platzer, M.
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18009. .18106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="FLAM_C repeat: matches 9. 17809. .17973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Alusx repeat: matches 27. 17043. .17169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="33 copies 2 mer tc 74% conserved"
14122. .14511
/note="MSTD repeat: matches 1. .394 of consensus"
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13342. .13761
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13007
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15987. .16255
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/note="match: GSS: Em:B32856"
13362. .13427
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PRI 05-FEB-2002

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REFERENCE
AUTHORS
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AC099798
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                                                                                                                                                                                                                                                             2 (bases 1 to 131328)
Waterston,R.H.
Direct Submission
Submitted (21-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                 Direct Submission
Submitted (03-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
    Center code: WUGSC Web site:http://gen
                                            Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                     3 (bases 1 to 131328) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Base-by-base quality values are not generally visible from GenBank flat file format but are available as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Quality Assessment: This entry has been annotate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of this entry's ASN.1 file.
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                                                                                                              63108,
Feb 3,
site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990329
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/db_xref="taxon:9606"
/chromosome="8"
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2002 this sequence version replaced gi:18056737.
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                                                                    Genome Center -----
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ne 7 clone RP11-559E21, complete sequence.
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hes 0;
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Seaman, S.,

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                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barra, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehbczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Nay, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 18, clone RP11-11F23
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Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roy,A., Santos,R., Schauer,S., Schupback,R., Sea
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/db_xref="taxon:9606"
/chromosome="7"
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FEATURES	AUTHORS	TITLE JOURNAL REFERENCE	TITLE JOURNAL REFERENCE AUTHORS
http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.washington.edu/RM/RepeatMasker.html  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project Information Center project name: L3150 Center clone name: 11_F_23 Location/Qualifiers	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhgh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., Macdonald, P., Major, J., Marquis, M., Matthews, C., Macchean, C., Macdonald, P., Major, J., Marquis, M., Natthews, C., Macchean, C., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Weneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rleback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Street, Cambridge, MA 02141, USA On Dec 10, 2001 this sequence version replaced gi:14269782. All repeats were identified using RepeatMasker:	poyusiny to hope of the party S. Fer Farry Marquis P. Marquis P. O'Donne g. P. Pierre Riley R.	Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission  Submitted (31-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 143799)  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, N., Bastier, V., Boundar, C., Lander, E., Allen, N., Anderson, S., Barren, N., Bastier, M., B
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RESULT 48
AC021765/c
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AC010998
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                            KEYWORDS
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                                          AC021765
AC021765.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-SEP-1999) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
3_(bases 1 to 146831)
                            HTG; HTGS_PHASE1;
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                                                                                      Homo
                                                                                                     AC021765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (09-AUG-2001) Genome Therapeutics Corporation, 100 Beaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome AC010998
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Data
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   1765 152393 bp DN7 sapiens clone RP11-9D19, WORKING
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9, 2001 this sequence version replaced gi:14717312.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /clone="RP11-95116"
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31937 c 31285 g 41777 t
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25505. .25550
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23628 ...23700
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tive 0; Mismatches
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Pred. No.
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Ne 10 clone RP11-95I16, complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen Anderson,S., Baldwin,J., Barda,N., Beckerly,R., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,, Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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Homo sapiens, clone RP11-9D19
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Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 152393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 146933 bases at least Q40 Consensus quality: 149520 bases at least Q30 Consensus quality: 150601 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
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Center clone name: 9_D_19
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                                                                                                                                                                                                                                                                                                                                            1 28910: contig of 28910 bp in length

28911 29010: gap of 100 bp

29011 31437: contig of 2427 bp in length

31438 31537: gap of 100 bp

31538 33952: contig of 2415 bp in length

33953 34052: gap of 100 bp

34053 38372: contig of 4320 bp in length
                                                                                                                                                                                                  38373 38472: gap of 100 bp
38473 81141: contig of 42669 bp
81142 81241: gap of 100 bp
                                                                                                           86895 86994:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
241: gap of 100 bp
86894: contig of 5653 bp in length
994: gap of 100 bp
95082: contig of 8088 bp in length
182: gap of 100 bp
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Collngelo,M., Collins,S., Collymore,A., Cook,A.,
                                                                                              Birren,B., Linton,L., Nusbaum,C. and Lander,E
Homo sapiens chromosome 17, clone RP11-145L16
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                AC104974.3 G1:18653683
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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129918 148772; contig of 18
148773 148872; gap of 10
148873 152393: contig of 39
10cation/Qualifiers
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81242. .86894
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31538. .33952
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/db_xref="taxon:9606"
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34053. .38372
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29011. .31437
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110147. .129817
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129918. .148772
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129817: contig of 19671 bp in length
9917: gap of 100 bp
148772: contig of 18855 bp in length
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Ginde, S., Gord, S., Goyette, m., January, M., Iliev, I., Johnson, K., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, K., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPhetters, R., Meldrim, J., McCarthy, M., McCarthy, M., Mordan, C., Mortou, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Schupback, 
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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, W.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the accession number will be preserved.

1 1709: contig of 1709 bp in
1710 1809: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and
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------ Project Information
Center project name: L22871
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Insert size: 152404; sum-of-contigs
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4561: contig of 1334 bp
100 hr
2 5811: cont:
     100 bp
9739: contig of 1378 bt
10 9839: gap of 100 bp
10 12205: gap of
1 12205: gap of
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1 3227: gap of 100
4561
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15911: gap of 1150 100 bp

7151: contin 100 bp
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3228. .4561
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47501. .53741
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72522. .84887
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/clone_lib="RPCI-11 Human Male BAC"
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99600: contig of 14613 bp in 10
99700: gap of 100 bp in 10
115353: contig of 15653 bp in 10
115453: gap of 100 bp in 10
131255: contig of 15802 bp in 10
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                                                                                                                                                                                                                                                  Submitted (24-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 15987)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Character, Cook, A., Cook,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP13-500A21
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                                                                                        Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fa
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 13, 2001 this sequence version replaced gi:17386327. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                  /note="<30 qual single clone coverage" 687. .719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Single clone coverage"
636. .642
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/chromosome="15"
/map="15"
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790. .794
                                                                                                                                                                     /note="Single clone coverage"
765. .770
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726. .761
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680. .686
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672. .679</pre>
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666. .671
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497. .527
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                        /note="<30 qual SNGL region"
1821. .1995
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       /rpt_family="CT~rich"
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/note="<30 qual SNGL region"
complement(2246. .2280)
/rpt_family="U2"
2350. .2539</pre>
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complement(3933. .4534)
/rpt_fami.
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/rpt_family="C-rich"
2050. .2130
/rpt_family="AluJb"
25022. .25376
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complement(7884. .79)
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complement(9157. .10047)
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10048. .10395
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8463. .8704
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/rpt_family="L2"
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/rpt_family="L2"
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RESULT 2
US-08-933-750C-66
; Sequence 66, Application US/08933750C
. Parent No. 5932442
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ARPLICANT: Flavier, Albert
APPLICANT: Gates, Krista
APPLICANT: Gates, Krista
APPLICANT: Wendland, Juergen
APPLICANT: Ayad-Durieux, Yasmina
APPLICANT: Dietrich, Fred
APPLICANT: Dietrich, Fred
APPLICANT: Philipsen, Peter
TITLE OF INVENTION: Fungal Target Genes and Methods
FILE REFERENCE: PB/S-30908A
CURRENT APPLICATION UMBER: US/09/588,256
CURRENT FILING DATE: 200-06-06
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(2382)
US-09-588-256-9
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 Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, P.
APPLICANT: Hillman
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                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9
LENGTH: 2382
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ORGANISM: Ashbya gossypii
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                1875 ggcttttgtgctaagttaact 1895
                                                                                                                                                             1990 ggcttttgtgctaagttaact 2010
                                                                                                                                                                                                                                                       Local Similarity
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Hillman,
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 Jennifer L.
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US-08-484-428-1
US-08-920-812-20
US-08-920-827-20
US-08-921-177-20
US-08-920-828-20
US-08-920-828-20
US-08-930-685-1
US-08-989-685-1
US-08-980-199-2
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US-09-176-228-4

US-09-176-228-4

US-09-688-376-1

US-09-130-114-1
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Pred. No.
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US-08-933-750C-66
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                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                           Sequence 66, Applications of the No. 6132973
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APPLICANT:
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ADDRESSEE:
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Query Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                         1419 cacacaggagagaagcctta 1438
                                APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/933,7:
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN RE
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                       1289 CACACAGGAGAGAGCCTTA 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line
IMMEDIATE SOURCE:
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LENGTH: 1892 base pairs
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA.
                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
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CITY: Palo Alto
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                                                                                                                     Shah, Purvi
Au-Young, Janice
                                                                                                      Yue, Henry
                                                                                                                                                         Hillman, Jennifer L.
Bandman, Olga
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Pred. No.
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3.4;
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SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/234,613

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COUNTRY:

USA

CA

94304

STREET: 3174 Porter Drive CITY: Palo Alto

COMPUTER: IBM CON OPERATING SYSTEM:

IBM Compatible

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98)..(523)
US-09-262-773-7
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-262-773-7

: Sequence 7, Application US/09262773

: Patent No. 6225451
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                                                                                                                                                                               APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION UNMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%; Sc
Best Local Similarity 100.0%; I
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Query Match
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APPLICATION NUMBER: US/08/933,750

APPLICATION NUMBER: 23, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ballinger, Dennis G. APPLICANT: Ding, Wei
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SEQUENCE CHARACTERISTICS:
LENGTH: 1892 base pairs
                                                                                                                                              LENGTH: 3240
TYPE: DNA
                                                                                                                             ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1419 cacacaggagagaagcctta 1438
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Pred. No. 3.4;
 Score 19;
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 DB 4;
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Length 3240;
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APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.

TITLE OF INVENTION: CHRONOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myrlad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 3244
TYPE: DNA
ORGANISM: human
                                                                                                                                             APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Ding, Wei
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
FITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
FITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SEGTH: 3264
TYPE: DNA
ORGANISM: human
FEATURE:
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; LOCATION: (98)..(2017)
US-09-262-773-3
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US-09-262-773-3
                                                                                     ; NAME/KEY: CDS
; LOCATION: (98)..(496)
US-09-262-773-5
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Best Local Similarity
Matches 19; Conserva
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                Query Match
Best Local Similarity
Matches
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                                                                                                                                      FEATURE:
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 Conservative
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                 0.7%; Score 19; DB 100.0%; Pred. No. 11;
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100.0%;
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; NAME/KEY: CDS
; LOCATION: (98)..(2041)
US-09-262-773-1
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0, 6225451
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Best Local :
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APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Warriad 3
FILE REFERENCE: Warriad 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/475,844
FILING DATE: 07-UN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,680
FILING DATE: 17-UN-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza
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Goodwin, Graham H.
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PCT-US95-08429-8
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; OTHER INFORMATION:
US-08-475-844-8
                                                                                            Sequence 8, Application PC/TUS9508429 GENERAL INFORMATION:
                                                                                                                                                                                                                Matches
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Matches 19; Conserv
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                      TITLE OF INVENTION:
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                                                           NUMBER OF SEQUENCES:
                                                                                 APPLICANT:
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LOCATION:
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LOCATION:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parmelee, Steven W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human CTCF cDNA
                                                                                                                                                                                                                                                                                                                 3810 base pairs
                                                                                                                                                                                                                                                                                                  1810
                                                                                                                                                                                                                                                                                                                                                                                          exon
1500..1649
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1380..1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
1246..1379
                                                                                                                                                                                                                Conservative
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
1075..1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
E: cDNA
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292..2475
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                                                                                                                                                                                                                                                                                                 ..1992
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                                                                                                                                                                                                                                                                                                                                                                                /label= exon6
                                                                                                                                                                                                                                                                                      /label= exon8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= exon3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= exon2
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                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                      2;
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                                                                                                                                                                                                               Indels
                                                                                                                                                                                                               0;
                                                                                                                                                                                                               Gaps
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PRIOR APPLICATION DATA:

CLASSIFICATION:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/I FILING DATE: 15-JUN-1995

PCT/US95/08429

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                        RESULT 10
US-09-262-773-206
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Sequence 206, Application US/09262773 Patent No. 6225451
                                                                                                                               Matches
                                                                                                                                            Query Match
Best Local 9
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                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 1075..1245
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 1810..19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon 1500..1649
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                           LOCATION: 1650..18 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                     NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 17-JUN-1994
                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
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                                                                                                                             1 Similarity 100.0%;
19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human CTCF cDNA
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1810..1992
----mTON: /label= exon8
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1380..1499
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281.
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292..2475
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                                                                                                                                                                                                                                                                                                              /label= exon6
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                                                                                                                                                                                                                                                                                                                                                                                                                    /label= exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= exon3
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                                                                                                                                                        0.7%;
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                                                                                                                                         Score 19; DB 5; Length 3810; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                  exon5
                                                                                                                               Mismatches
                                                                                                                               0; Indels
                                                                                                                               0,
                                                                                                                             Gaps
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; TYPE: DNA
; ORGANISM: human
US-09-262-773-9
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; ORGANISM: human
US-09-262-773-206
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APPLICANT: Ballinger, Den
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susann
APPLICANT: Hess, Mark A.
                                                                                                                                                                                                                                                                       Db 14681 tcagacatcagaggacaca 14699
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                                                                                                                                                                                                                    RESULT 12
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CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 206
LENGTH: 20137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 9
LENGTH: 20138
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Best Local :
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                Sequence 210, Application US/09262773 Patent No. 6225451
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
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                APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORTITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/262,773 CURRENT FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14680 tcagacatcagaggacaca 14698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ding, Wei
CURRENT APPLICATION NUMBER: US/09/262,773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ballinger, Dennis G.
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                                                      CHROMOSOME 11-LINKED CORONARY HEART DISEASE
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100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                             0,
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CURRENT FILING DATE: 1999-03-04

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VER. 2.0

SEQ ID NO 210

LENGTH: 23071

TYPE: DNA

ORGANISM: human
US-09-262-773-210
                                                            ; OTHER INFORMATION: US-08-724-394A-20
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Megabase Transcript Map: TITLE OF INVENTION: Sequences and Antibodies NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2068 tcagacatcagaggacaca 2086
                                                                                                                                    TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 19; Conserv
                                                                                        NAME/KEY: misc_feature LOCATION: 1..246240
                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarca
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                               LENGTH:
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94111-3834
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                                                                                                                                                                                            246240 base pairs
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Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruddy, David A.
                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feder, John N.
                                                                                                                                                                                                                                                           415-576-0200
                                                                                                                                      CDNA
                                                                                                                                                                not relevant
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100.0%; Pr
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100.0%;
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Pred. No.
 Score 19;
Pred. No.
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10;
 DB 2;
10;
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               Length 246240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 15
US-08-724-394A-22/c
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                                                                                                                                                                                                                                 US-08-724-394A-21
Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                              2298 tttcaggagccctgccctt 2316
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TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0:
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Tsuchihashi, Zenta
Wolff, Roger K.
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100.0%; Pr
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Sequences and Antibodies
31
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Pred. No.
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US-08-507-016-8
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Best Local Similarity 100
Matches 19; Conservative
                                                                                                                                                                                                       Sequence 8, Application US/08507016 Patent No. 5756460
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              36115 TTTCAGGAGCCCTGCCCTT 36097
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INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: not
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                  APPLICANT: SHINE, JOHN
TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING
TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
                                                                                                                                                                                                                                                                                                                              2298 tttcaggagccctgccctt 2316
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LENGTH: 246240 base pa
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megabase Transcript Map: NO. 58
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                               NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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LOCATION: 1.24624
OTHER INFORMATION:
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                                CITY:
                  STATE:
                                               STREET:
COUNTRY:
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                              WASHINGTON
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                                               E: ROTHWELL, FIGG, ERNST & KURZ
555 THIRTEENTH STREET, N.W.
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USA
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                                                                                                                                                                    EVANS, HELEN F.
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1..246240
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US-09-303-524A-1/c
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US-09-303-524A-1
                                                                       SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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Best Local Similarity 100
Matches 18; Conservative
                                                                                                                                                                                                                  APPLICANT: CHAMBERS, JONATHAN K.
APPLICANT: STEWART, BRIAN R.
APPLICANT: AMES, ROBERT S.
APPLICANT: SARAU, HENRY M.
APPLICANT: FOLEY, JIM
APPLICANT: FOLEY, JIM
APPLICANT: ARNOLD, ANNE ROMANIC
APPLICANT: NUVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/AU92/
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: AU PK4953
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
                                                                                                        PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-(
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/303,524A CURRENT FILING DATE: 1999-04-30
                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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INFORMATION FOR SEQ ID NO:
             LENGTH: 1027
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1553 cctgaagtcaaaccttaa 1570
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 575 base pairs
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LOCATION:
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25-JULY-1995
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Pred. No.
                                                                                                                                                                                                                    OF THE INTERACTION BETWEEN THE HUMAN KIAA0001 LIGANDS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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32;
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RESULT 19
US-08-820-170A-11
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US-08-416-870C-9
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Sequence 11, Application US/08820170A
                                                                                                                                                  Matches
                                                                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: HIYOSH
                                                                                    1175 TGTGGGCAAGGCTTTTGT 1192
                                                                                                   1866 tgtgggcaaggcttttgt 1883
                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TYSON, ROBERT HUW
APPLICANT: PAGE, ANTHONY MILES JOHN
APPLICANT: PAGE, ANTHONY MILES JOHN
TITLE OF INVENTION: DA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT V
TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                            LENGTH: 1558 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                  18;
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Pred. No.
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Pred. No.
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                                                                                                                                                                DB 1;
32;
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32;
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US-09-055-699-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: DC-DOS/MS-DOS
               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                        APPLICANT: Toyomasa, KATAGIRI TITLE OF INVENTION: HUMAN GENE
                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                      APPLICANT:
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APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KAT
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APPLICANT:
                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                        STREET: 2100 Penr
CITY: Washington
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Washington
STATE: D.C.
                                                                                                                                            STATE:
                                                                                                                           COUNTRY:
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APPLICATION NUMBER:
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                                                                                                           RY: United States
20037-3202
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2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                        Takeshi, WATA
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WATANABE
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WATANABE
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US/09/055,699
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                              Version #1.30
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32;
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CÜRRENT APPLICATION NUMBER: US/09/273,565A
CÜRRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: 08/020,170
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: JP 63410/1996
EARLIER APPLICATION NUMBER: JP 63410/1996
EARLIER FILING DATE: 1996-03-19
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US-09-565-538-11
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Sequence 11, Application US/09:
Patent NO. 6333404
GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 11
LENGTH: 2133
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Patent No. 6166190
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                            Matches
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APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBLOUTTIN-CONJUGATING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: JP 69163/1997
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
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TELECHRONE: (202) 293-7060
TELECRAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                              MOLECULE TYPE: DNA(genomic)
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LENGTH: 2133 base pair
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                        Application US/09565538
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100.0%; Pr
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Pred. No.
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US-08-820-170A-12
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PRIOR FILING DATE: 1999-03-22
PRIOR PELICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
                                                                                                                                       CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5831058 GENERAL INFORMATION:
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Matches 18; Conservative
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LENGTH: 2133
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CURRENT FILING DATE: 2000-05-05
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ORGANISM: Homo sapiens
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1493 caggggagaaaccttatg 1510
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA(geno HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                   LENGTH:
                                                                         nucleic acid
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Takeshi, WATANABE
Masato, HORIE
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                     DNA (genomic)
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RESULT 24
US-09-055-699-12
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                                                       US-09-055-699-12
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                            TELEFAX: (202) 293-786
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
IMMEDIATE SOURCE:
LIBRARY: Human fetal brain cDNA library
CLONE: GEN-076C09
                                                                                                           IMMEDIATE SOURCE:
   LIBRARY: Human fetal brain cDNA library
   CLONE: GEN-076C09
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1838 CAGGGGAGAAACCTTATG 1855
                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                 CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington : D.C.
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6005088
                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                3754 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                                                                                                                      NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toyomasa, KATAGIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takeshi, WATAI
Masato, HORIE
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346..2478
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Takeshi, WATANABE
                                                                    CDS
346..2478
                                                                                                                                                                                          linear
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                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                       single
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0.6%;
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 Score 18;
Pred. No.
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Pred. No
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DB
32;
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             Length 3754;
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; NAME/KEY: CDS
; LOCATION: (346)..(2478)
US-09-273-565-12
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APPLICANT: FUJIWARA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 12
LENGTH: 3754
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Appli
Patent No. 6333404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                  PRIOR APPLICATION NUMBER: 09/273,565
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/565,538
CURRENT FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING EFFILE REFERENCE: 07-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
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APPLICANT: WATANABE, TAKI
APPLICANT: HORIE, MASATO
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1996-03-19
EARLIER APPLICATION NUMBER: JP 69163/1997
EARLIER FILING DATE: 1997-03-05
                                                           PRIOR APPLICATION NUMBER: JP 63410/1996 PRIOR FILING DATE: 1996-03-19
                                                                                                                                                                                                                                                                         FILE REFERENCE: Q-53599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: JP 63410/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 08/820,170
                     PRIOR FILING DATE: 1997-03-05
                                        PRIOR APPLICATION NUMBER: JP 69163/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1087 caggggagaaaccttatg 1104
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                                                                                                                                                                                                                                                                                                                                HORIE, MASATO
                                                                                                                                                                                                                                                                                                                                                        WATANABE,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09565538
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NOS: 95
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
32;
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RESULT 28
US-09-060-836-2/c
; Sequence 2, Application US/09060836
; Patent No. 5981707
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US-08-751-189-2/c
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; LOCATION: (346)..(2478)
US-09-565-538-12
                                                                                                                                                                                                                                             US-08-751-189-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08751189 Patent No. 5919656
                                                                                                                                                                Matches
                                                                                                                                                                                            Query Match
                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                              1838 caggggagaaaccttatg 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 591965661 Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1087 caggggagaaaccttatg 1104
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                                                                                                                              2553 tttttacactgctgtgcc 2570
                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1840 De Havi
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/751,189
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Oleski, Nancy A. REGISTRATION NUMBER: 34,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                             Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Amgen, Inc.
1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                         7886 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                Conservative
                                                                                                                                                                               0.6%; Score 18;
100.0%; Pred. No
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Pred. No.
                                                                                                                                                                Mismatches
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                                                                                                                                                                                NO.
                                                                                                                                                                             DB 2;
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 3754;
                                                                                                                                                                                            Length 7886;
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RESULT 29
US-09-184-445-2/c
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Best Local Similarity 100.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 7886 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7660 TTTTTACACTGCTGTGCC 7643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/751,189
FILLING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2553 tttttacactgctgtgcc 2570
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                            ZIP: 91320-1789
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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    APPLICATION NUMBER:
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US/09/184,445
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                                          Version
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/751,189 FILING DATE: 15-NOV-1996

CLASSIFICATION:

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ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-43
                                                                            TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7886 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
                                                                                                                                                                                           APPLICATION NUMBER: GB 9009549.8 FILING DATE: 27-APR-1090 ATTORNEY/AGENT INFORMATION: NAME: FOX. SAM L
                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROTHLEIN, ROBERT APPLICANT: APHALR, JOHN R APPLICANT: ATHMAL, DILJEET S TITLE OF INVENTION: HUMANIZEI
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V Match 0.6%; So Local Similarity 100.0%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: POFILING DATE: 19910429
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                               LENGTH:
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                                             NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Ave. NW Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                  linear
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                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
DNA (genomic)
                                   both
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Pred. No.
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Query Match

0.6%;

Score 17;

DB 5;

Length 80;

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US-08-956-182-21/c
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                                                                                                                                                                                     RESULT
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                                                                                                                   Sequence 124, Application US/08592126 Patent No. 5821091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEO ID NO: 21
                                                         APPLICANT: Gregory DO TITLE OF INVENTION: TITLE OF INVENTION: INUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                            2101 tttatgtgtatagggaa 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 273 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL SEED SPECIF
                                                                                                                                                                                                                               650 agactccagactcctgt 666
              STREET:
                                                                                                                                                                                                                                                                                             Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AGACTCCAGACTCCTGT 27
                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/956,182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11530
                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
: 350 Cambridge Avenue, Suite 250 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                        Gregory Dolganov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                             Conservative
                           Dehlinger & Associates
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NOVEL SEED SPECIFIC PROMOTERS BASED ON
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                                                             Polypeptides
151
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                                                                                         Transcripts Encoding Immunomodulatory
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; Mismatches
                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                          DB 3;
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                                                                                                                                                                                                                                                                                                                          Length 273;
                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:

94306

USA

MEDIUM TYPE:

Floppy disk

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; ORIGINAL SOURCE: ; INDIVIDUAL ISOLATE: G45.seq US-08-592-126-124
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-905-223-133
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 324-096
INFORMATION FOR SEQ ID NO:
       FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSEN, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                               APPLICANT: Duelert, APPLICANT: Lacroix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: 1
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LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTURNEY/AGENT INFORMATION:
                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 tggagagaggagagaaa 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 TGGAGAGAGAGAGAAA 246
                                                                                                                                                                                                                                STREET: bul well
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      APPLICATION NUMBER:
                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: Win95
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                               92101-3505
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                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                       501 West Broadway
                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                             Duelert, Aymeric
                                                                                                                                                                                                                                                                                                                                                              Edwards, Jean-Baptiste D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                    Word
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100.0%; Pr
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                                                                                        US/08/905,223
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Pred. No.
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; IDENTIFICATION METHOD: Von Heijne matrix ; OTHER INFORMATION: SCORE 4.1 ; OTHER INFORMATION: SEG VMLETCGLLVSLG/HP US-08-905-223-133
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                                                                                                                                           ; OTHER INFORMATION: n = A,T,C or G US-09-328-111-648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
US-09-328-111-648
                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 648 LENGTH: 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
                                                     Best Local Similarity Matches 17; Conserv
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 626233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 648,
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE Transcription or Carlo INAL SOURCE:
ORGANISH: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Steinmann, Kathleen APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 133:
                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1998-06-10 NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Endege, Wilson O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Derti,
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)...(532)
                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '294 gaggtgatgctggagac 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 347 base pairs
TYPE: NUCLEIC ACID
1251 cacactggggagaagcc 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 GAGGTGATGCTGGAGAC 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide LOCATION: 183..338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                     100.0%;
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100.0%; Pred. No.
                                                                     0.6%; Score 17;
100.0%; Pred. No.
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                                                       Mismatches
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cacactggggagaagcc 270

Sequence 433, Application US/09385982
Patent No. 6262334

·09-385-982-433/c

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US-08-956-182-16/c

: Sequence 16, Applicati

: Patent No. 6100450

: GENERAL INFORMATION:
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; LOCATION: (1)...(563)
;- OTHER INFORMATION: n = A,T,C or
US-09-385-982-433
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Best Local Similarity
Thes 17; Conserv
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EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/385,982 CURRENT FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOCUCTS: II
TILE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 563
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10701
                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1419 cacacaggagagaagcc 1435
TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                              APPLICATION NUMBER: US/08/956,182
                                                                                                                                                                                                                                                                                11530
                                                                                                                                                                                                                                                                                                                 Garden City
: New York
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                                                                                                                                                                                                                                                                                                                                                   E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                          Terry L.
NOVEL SEED SPECIFIC PROMOTERS
ARABIDOPSIS GENES
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Pred. No.
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                                                                                                                                                                                    Version #1
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APPLICANT: Baker, Adam
APPLICANT: Cotten, Matthew
APPLICANT: Cotten, Matthew
APPLICANT: Chiocca, Susanna
APPLICANT: Kurzbauer, Robert
APPLICANT: Kurzbauer, Robert
APPLICANT: Schaffner, Gotthold
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800000
CURRENT APPLICATION NUMBER: US/09/171,461
CURRENT FILING DATE: 1999-01-12
EARLIER APPLICATION NUMBER: PCT/EP97/01944
EARLIER FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)..(1362)
US-09-171-461-47
                                                                                                                                                                                         RESULT 38
US-07-662-007B-38/c
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                                                                                                                                                        Sequence 38, Application US/07662007B Patent No. 5344771
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LENGTH: 1362
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Best Local
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                          GENERAL INFORMATION:
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: CELO VIRUS
FEATURE:
                                                                          APPLICANT: Davies, num.....APPLICANT: Pollard, Michael Roman APPLICANT: Voekler, Toni Alois
                                                                                                                                                                                                                                                                       1028 ggaatgtgggcgaggct 1044
                                                    APPLICANT: Voekler, Toni Alois
APPLICANT: Thompson, Gregory A.
TITLE OF INVENTION: Plant Thioesterases
                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                      746 ggaatgtgggcgaggct 762
                                                                                                                                                                                                                                                                                                                   Local Similarity hes 17; Conserv
 STREET:
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                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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E: Calgene, Inc.
1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 base pairs
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Pred. No.
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07/773,096

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RESULT 39
US-07-968-971A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07968971A Patent No. 5455167
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,883 aggagtcaaacctcctt 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31.845
REFERENCE/DOCKET NUMBER: CGNE 70-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/6:
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: MicrosoftWord 4.0
CURRENT APPLICATION DATA:
           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
                                                                                                            COMPUTER: Apple Macintosh 6.0.7 OPERATING SYSTEM: Macintosh 6.0.7 SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Toni A. Voelker
APPLICANT: Huw Maelor Davies
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             ADULT STREET: LIVER DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       969 AGGAGTCAAACCTCCTT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/5 FILING DATE: 26-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199104
                                                                              APPLICATION NUMBER: UPFILING DATE: 19921030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 17; Conserv
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                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                          Diskette, 3.50 inch, 1.0 MB
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                                                                                             US/07/968,971A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17;
Pred. No.
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99;
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US-07-824-247-38/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                          COMPUTER: Apple Macintosh 6
OPERATING SYSTEM: Macintosh 6
SOFTWARE: MicrosoftWord 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/824
FILING DATE: 19920122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19920122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                            FILING DATE: 24-OCT-199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/
FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       969 AGGAGTCAAACCTCCTT 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 3:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/
FILING DATE: 7-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 21-MA
 APPLICATION NUMBER: FILING DATE: 21-MA
                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 95616
                                                                                                                                                                                                                                                                                                                                           CITY: Davis
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                          California
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                                                                                                                                                                                                                                                                                                             USA
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(916) 753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA to mRNA
                                                                                              24-OCT-1991
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22-JAN-1992
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JMBER: 07/704,861
21-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%;
                                                                                                                                                                                                                               Macintosh 6.0.7
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                                                               07/773,096
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                                                                                                                                                                                                                                                             3.50 inch,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                         720 KB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1561;
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Gaps

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RESULT 41
US-07-824-247-41/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                   SOFTWARE: MicrosoftWord 4.0 CURRENT APPLICATION DATA:
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
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APPLICATION NUMBER: 07/620,426
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
                                                PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/704,861 FILING DATE: 21-MAY-1991 RIOR APPLICATION DATA:
                                                                                                                                                                                    APPLICATION NUMBER: UPFILING DATE: 19920122
                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 26-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative 0;
                                                                                                                                                                                                                                                                                                                       95616
                                                                                                                                                                                                                                                                                                                                                                      Davis
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                                                                                                                                                                                                                                                                                                                                                   California
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                                                                                                                                                                                                                                                                                   3.50 inch,
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Pred. No.
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                                                                                                                                                                                                                                                                                   720
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99;
                                                                                                                                                                                                                                                                                   KB storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pair
                                                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04332
FILING DATE: 21-MAY-1992
FILING DATE: 800
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Voelker, Toni Alois APPLICANT: Davies, Huw Maelor TITLE OF INVENTION: Plant Thios NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/514,030 FILING DATE: 26-APR-1990 ATTORNEY/AGENT INFORMATION:
                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA to mRNA
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OPERATING SYSTEM: Macintosh 7
SOFTWARE: Microsoft Word 5.1a
                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                            STREET: 192
CITY: Davis
CLASSIFICATION:
                                                                                                                                                     APPLICATION NUMBER: US/08/142,473A FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 95616
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TOPOLOGY: li
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              22-JAN-1992
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                              07/824,247
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                         720 KB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1561;
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REGISTRATION NUMBER:

31,845

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Best Local S
Matches 17
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Sequence 1, APP-
5667997
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   883 aggagtcaaacctcctt 899
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APPLICANT: I
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REFERENCE/DOCKET NUMBER: CGI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
TELEPAX: 916-753-1510
        FILING LAND.: 435
CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: USSN 07/968,971
APPLICATION NUMBER: 30 October, 1992
                                                                                                                                                                                                                                                                                             ADDAL
STREET:
CITY: Davis
TR: CA
                                                                                                                   FILING DATE: 26 Apri-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 15
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NAME: Elizabeth Lassen
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APPLICATION NUMBER: 07/7
FILING DATE: 21-MAY-1991
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Davies, Huw Maelor
APPLICANT: Knutzon, Deborah S.
TITLE OF INVENTION: Medium Cha
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         969 AGGAGTCAAACCTCCTT 953
                                                                                        APPLICATION NUMBER: PCT/UFILING DATE: 29 October,
                                                                                                                                                                                                             COMPUTER: Apple Macintosh 7.0 OPERATING SYSTEM: Macintosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-OCT
                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                  APPLICATION NUMBER: US/08/424,406
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Elizabeth
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1920 Fifth Street
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N: 435
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                                                                                        PCT/US93/10814
ober, 1993
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Pred. No.
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Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Deborah Hawkins
APPLICANT: Aubrey Jones
TITLE OF INVENTION: Plant Acyl
TITLE OF INVENTION: Sequences
NUMBER OF SEQUENCES: 33
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13131
FILING DATE: 10-NOV-1994
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                                                         APPLICATION NUMBER: 08/20
FILING DATE: 16-JUN-1994
ATTORNEY AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34/
                                                                                                                         FILING DATE: 10-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,695
                                                                                                                                                                      PRIOR APPLICATION DATA: 08/152,004
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
REFERENCE/DOCKET NUMBER: CGNE 100-1WO TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: Macinto
SOFTWARE: Microsoft Word
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CITY: Davis
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                                REGISTRATION NUMBER:
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5. 5723761
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1920 Fifth Street
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Jean Kridl
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Pred. No.
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Best Local Similarity
Matches 17; Conserv
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TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
07/782,263
                                                                                                                                                                     FILING DATE: 24-OCT-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/824,247
FILING DATE: 22-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUN-1>>-
FILING DATE: 08-JUN-1>>-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR OB/142,473
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CORRESPONDENCE ADDRESS:
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                                                            ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
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                                                                                          APPLICATION NUMBER: 07/7
FILING DATE: 21-MAY-1991
                                                                                                                                       APPLICATION NUMBER: 07/773,096 FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/I
FILING DATE: 21-MAY-1992
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                                                                                                                                     FILING DATE:
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                                   NAME:
                                               REGISTRATION NUMBER:
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NUMBER: 34
J. Schwedler
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                                              31,845
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Pred. No.
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99;
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GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                       APPLICATION NUMBER: 07/782,263
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                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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LENGTH: 1561 base pair
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MEDIUM TYPE: Diskette,
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APPLICANT: Davies, Huw Maelor
TITLE OF INVENTION: Plant Med
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                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/142,473 FILING DATE: 18-NOV-1993
                REGISTRATION NUMBER:
                                            REGISTRATION NUMBER:
                                                                                           FILING DATE:
                                                                                                                                    FILING DATE:
                                                                                                                                                 APPLICATION NUMBER: 07/773,096
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95616
                                Donna
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                                                         Elizabeth Lassen
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                              E. Scherer
                                                                                           21-MAY-1991
                                                                                                                                                                              24-OCT-1991
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Schwedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Medium-Chain Thioesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toni Alois
                                                                                                                                                                                                                                                                                                                                                                                                                                   Macintosh
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                                                                                                       07/704,861
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                                         31,845
                34,719
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Pred. No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38,
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INFORMATION FOR SEQ ID NO: 1:
                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,007
APPLICATION NUMBER: 27-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh IIC1
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1a
CURRENT APPLICATION DATA:
        FILING DATE: 30-NOV-1230
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/514,030
                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7
FILING DATE: 21-MAY-1991
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
07/782,263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
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                                                                                                                                      APPLICATION NUMBER: PCT/US91/02960 FILING DATE: 25-APR-1991
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/7 FILING DATE: 24-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                             APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/824,247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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linear
                                                                                                                                                                                                                                                                                                                                           22-JAN-1992
                                                                                                                                                                                                                                    7-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-95
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26-APR-1990
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                                                             07/620,426
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Pred. No.
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                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
07/782,263
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,007
FILING DATE: 27-FEB-1991
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/:
FILING DATE: 7-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Voelker, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1561 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 916-753-6313
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 22-JAN-1992
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                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                           APPLICATION NUMBER: 07/70 FILING DATE: 24-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh IIci
OPERATING SYSTEM: Macintosh 7.
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                                                                       APPLICATION NUMBER: FILING DATE: 25-API
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CITY: Davis
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APPLICATION NUMBER:
                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        95616
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1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916-753-1510
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                                                                                                                   21-MAY-1991
                                                                        25-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toni Alois
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                                                                                                                                 07/704,861
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                                                                                     PCT/US91/02960
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07/620,426
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Pred. No.
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FILING DATE:

30-NOV-1990

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US-08-933-750C-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53, Application US/08933750C
Patent No. 5932442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                       APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      969 AGGAGTCAAACCTCCTT 953
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                                                                                                                                                                                                  COMPUTER: IBM CONTROPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                            FILING DATE:
                                                                                                          APPLICATION NUMBER:
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TELEPHONE:
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T: Corley, Neil C.
INVENTION: HUMAN R
                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                            USA
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US-09-234-613-53
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                                                                                                                                         APPLICATION NUMBER: US/08/933
FILING DATE: September 23, 19
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
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LENGTH: 2031 base pairs
TYPE: nucleic acid
                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2031 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskette
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               IMMEDIATE SOURCE:
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TELEFAX: 415-845-4166
                                       STRANDEDNESS:
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CLASSIFICATION:
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LIBRARY:
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3174 Porter Drive
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Bandman, Olga
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September 23, 1997
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